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Result
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Human Hepatocyte g Human hepatocyte g	AAR21976 AAR52942	13 14	728 728	8.4		4061 4061	44 45
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-II. Þ	AAR29819	13	723	•		0	41
Human hepatocyte g	AAG68090 AAB84517	22	728			4066	40 40
a	AAW97041	20	728	•		4066	38
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Human leukocyte-de	AAW59923	19	723			4078.5	34
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Human plasminogen-	AAW76690 AAR21142	139	723 723			~ ~	30
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Vascular endothelial cell growth factor protein - used for promoting angiogenesis in the treatment of cardiac angiopathy, wounds, burn injuries, postoperative tissue damage etc. Enhance; growth; vascular endothelial cell; human; tumour; cell line; HUOCA-II; HUOCA-III; blood vessel; wounds; burns; decubitus; post-operative tissue damage; drug; cardiac angiopathy. WPI; 1993-215669/27. N-PSDB; AAQ45702. Adachi M, (TERU) TERUMO 28-NOV-1991; 27-NOV-1992; 07-JUL-1993 EP550296-A. Homo sapiens Harada K, CORP. 91JP-0337999 92EP-0403199 Hirahara I, Sudo

Vascular endothelial cell growth enhancer protein.

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Pred. No. 9.5e-277;
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Best Local S
Matches 728
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                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the human hepatic parenchymal cell growth factor (HGF), which has a molecular weight of 76-92 kD estimated by SDS-PAGE, parenchymal cell growth activity, which is lost following heat treatment at 80 degrees C for 10 minutes and strong affinity towards heparin. It may be used to treat and prevent ischaemic diseases, e.g. blood reperfusion disorder, is chaemic reperfusion disorders in liver transplant, acute liver failure and organ disorder during organ transplant. For adults, it is administered at a level of 1 microg to 10 mg/kg/day, preferably 10-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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ischaemia; ischaemic; disease; reperfusion; disor
r; transplant; acute; failure; ischemia; ischemic;
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Pred. No. 9.5e-277;
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                                                                                                                                                                                                         /note=
487..60
                                           /label=
211..288
                                                                                                                                                                                                                                                                               Location/Qualifiers 494..495
                                                                                            /note= "Hydrophobic 128..206
                                                                                                                                                             /note= "prepro-sequence"
                        /label=
                                                                                                                                                                                                                                                       /label= Proteolytic_cleavage_site
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This sequence represents the wild type full length sequence of human CC hepatocyte growth factor (HGF). HGF is isolated from human serum CC and is a disulphide linked heterodimer derived by proteolytic cleavage of this pro-hormone form between residues 494 and 495. This generates a CC molecule composed of an alpha-subunit of 440 amino acids (mol. wt. 69 CC kD) and a beta-subunit of 234 amino acids (mol. wt. 34 kD). The alpha CC and beta subunits are encoded by a single open reading frame. The alpha CC subunit contains four kringle domains based on their homology to kringle-like domains in other proteins, e.g. prothrombin, plasminogen. CC kringle-like domains in other proteins, e.g. prothrombin, plasminogen. The beta subunit shows high homology to the catalytic domain of serine proteases. However two of the three residues which form the catalytic contains four the other proteases are not conserved in HGF. Therefore, the precise function of the beta chain remains unknown. The invention includes HGF variants which retain HGF receptor binding activity without having the biological activity of wild-type HGF. They can be used for the treatment of pathological conditions associated with the activation of a HGF receptor schivation.
Query Match
Best Local Sin
Matches 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-1993;
18-MAY-1992;
18-MAY-1992;
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                                                               Sequence
                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                      New hepatocyte growth factor variants - are resistant to proteolytic cleavage into a 2-chain form, useful as HGF a
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Conservative
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            11-JUN-1990;
                                 07-JUN-1991;
                                                                                                                      diagnosis;
                                                                                                                         Hepatocyte-derived growth factor; HGF; human; liver; hepatoma;
                                                      19-AUG-1998
                                                                          EP859009-A2
                                                                                                                                                   Human leukocyte-derived hepatocyte growth factor HCL3
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ETTECIOGOGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS

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C hepatocyte growth factor (HGF) HLC3, deduced from a cDNA clone
C (see AAV53626) obtained from a leukocyte cDNA library. Another
C leukocyte-derived HGF, HLC2 (see AAW5923), was identified that
C differs from HLC3 by having amino acid residues 162-166 deleted.
C a claimed method of producing a HGF comprises: transforming
C mammalian cells (preferably CHO cells) with a recombinant
C expression vector that has a promoter (preferably the SV40 early
C promoter), a gene coding for human leukocyte-derived HGF, and the
C dilydrofolate reductase gene; (b) culturing the transformed cells
C methotravate; and (c) recovering the HGF polypeptide from the
C culture supernatant. HGF polypeptides may be used as hepatocyte
C research on liver function, research on the action of various
C hormones and drugs on hepatocytes, research on the carcinogenesis
C mechanism of hepatoma, clinical diagnostic reagents using an
antibody against the polypeptide and therapeutic drugs for liver
                                                                                                                                                                                                                                                            Matches
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Best Local
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              HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL
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Pred. No. 9 5e-277;
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                                                                                                                                                                                                                                                                                                                                     preventive and/or treating agent - comprises hepatocyte
tor, used for diseases caused by high blood sugar
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Pred. No. 9.5e-277;
Mismatches 0;
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) AZUMA H.
) MITSUBISHI CHEM (
) MIYAZAKI KEN.
) TSUBOUCHI H.
                                                                                                                                                                                                          utic; drug; hepatic hepatitis.
                                                                                                                                                                                                                                                                                                                                                   standard; protein; 728
                                                                                                                                                                                                                                                                   human
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                                                                                                96JP-0163063
                                                                                                                                                                                                                         factor; HGF; W/O/W emulsion; blood half hepatic tissue; hepatic disease; acute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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Pred. No. 9.5e-277;
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Best Local Similarity
Matches 728; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
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ETTECIQGQEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS
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ive agent; therapeutic agent; glycogen;
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                                                                              Side effect inhibitor for cancer therapy - growth factor and inhibiting side effects r treatment by chemotherapy, radiotherapy
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      inhibit side effects in treating cancers by chemotherapy radiotherapy, etc. With it, it is possible to conduct mu cancer therapy and to improve the carcinostatic effects. extremely useful in the field of clinical medicine.
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Best Local
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See also AAR25676-92, AAQ26713-27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant human hepatocyte growth factor and DNA encoding useful for diagnosis and treatment of hepatic disease and transgenic animal prepn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 11; 28pp; Japanese.
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                                                        DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRD
                                                                                                                                                    ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME 420
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                                           dhpviscaktkqlrvvngiptrtnigwmvslryrnkhicggslikeswvltarqcfpsrd
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lkdyeawlgihdvhgrgdekckqvlnvsqlvygpegsdlvlmklarpavlddfvstidlp
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Pred. No. 2.9e-276;
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                                                                   The gene encodes an inhibitor of HGF, which has a molecular weight of ca. 76000 to 92000 as determined by SDS-PAGE. Human modified (NP) HGF-A and -B fragments were prepared from human HGF CDNA. This was amplified by PCR to give a human NP-HGF DNA fragment that was transformed into E.coli. (see AAQ47833) for a related sequence
                                                   Sequence
                                                                                                                                                     New protein is competitive inhibitor of hepatocyte - used in animal model of liver disease
                                                                                                                                                                                    WPI; 1993-297806/38.
N-PSDB; AAQ47832.
                                                                                                                                Claim 7; Page 8-11; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                  Key
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liver disease.
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         99.8%;
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Score 4119; DB 14;
Pred. No. 2.9e-276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agent contg. hepatocyte growth factor treating renal diseases and promoting diagnostic for renal diseases
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27; Conservative
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99.9%;
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                                                                                                                         The present sequence represents a human hepatocyte growth factor (HGF) variant. The HGF variants of the invention bind to the HGF receptor, but are substantially unable to bind heparan sulphate proteoglycan. The HGF variants are useful in medicine e.g. variants having the same effects on while antagonistic variants can be administered to patients requiring HGF, antagonists. They are especially useful for treating cancer. Some of the mitogenic activity than wt-HGF in rats. They are therefore useful give greater therapeutically as wt-HGF, but may have superior effects in vivo, e.g. give greater tissue penetration and ability to reach cell or tissue
                                                                                      Sequence
                                                                                                                                                                                                                                                   Claim 6; Page ~; 75pp; English.
                                                                                                                                                                                                                                                                 Hepatocyte growth factor variants - binding to hepatocyte growth factor receptor, useful in medicine e.g. for cancer therapy
                                                                                                                                                                                                                                                                                                     WPI; 1999-024213/02
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heparan sulphate proteoglycan; cancer.
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99.7%;
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Pred. No. 4.7e-276;
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Best Local Similarity
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11-AUG-1989;
03-APR-1990;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pKCRHGF-2. This is used to transform host cells for recombinant expression of the human hepatic parenchymal cell growth factor (hHGF). hHGF is useful in the treatment of hepatic diseases, e.g. cirrhosis. It is produced in large amts., stably using this method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatic parenchymal cell growth factor - promethods, useful for e.g. treating cirrhosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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DB; AAQ10489.
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5.5e-276;
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                The present sequence represents a human hepatocyte growth factor (HGF) variant. The HGF variants of the invention bind to the HGF receptor, but are substantially unable to bind heparan sulphate proteoglycan. The HGF variants are useful in medicine e.g. variants having the same effects on target cells as wt-HGF can be administered to patients requiring HGF, while antagonistic variants can be administered to patients requiring HGF, while antagonists. They are especially useful for treating cancer. Some of the variants have a longer circulatory half-life in vivo and a greater mitogenic activity than wt-HGF in rats. They are therefore useful therapeutically as wt-HGF, but may have superior effects in vivo, e.g.
                                                                                                                                           Disclosure;
                                                                                                                                                                Hepatocyte growth factor variants - binding to hepatocyte growth factor receptor, useful in medicine e.g. for cancer therapy
                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                       Birchmeier W,
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          Human leukocyte-derived HGF
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                                   espwcfttdpkirvgycsqipncdmshgqdcyrgngknymgnlsqtrsgltcsmwdknme
                                             ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME
                                                                       etteciqgqgegyrgtvntiwngipcqrwdsqyphehdmtpenfkckdlrenycrnpdgs
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
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ALIGNMENTS

A:Molecule type: mRNA
A:Residues: 1-161,167-728 <SE4>
A:Cross-references: EMBL:X16323
A:Experimental source: leukocyte
R:Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nak
Blochem. Biophys. Res. Commun. 163, 967-973, 1989
A:Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth
A:Reference number: A33512
A:Accession: A33512 A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936 R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asam: Biochem. Biophys. Res. Commun. 172, 327, 1990 A;Title: Isolation and expression of cDNA for different forms of hepatocy A;Reference number: A36677; MUID:91025062 A;Accession: B36677 A;Molecule type: mRNA A;Residues: 1-728 <SE3> R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growt A;Reference number: A41140; MUID:91334393
A;Accession: A41140. A;Cross-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991 Gene 102, 213-219, 1991 A;Title: Organization of the human hepatocyte growth factor-encoding gene A;Reference number: JH0579; MUID:91340155 A;Accession: JH0579 A:Description: Organization of the human hepatocyte growth factor-encoding A:Reference number: JU0333 A; Molecule type: MKNA A; Molecule type: MKNA A; MOlecule type: MKNA A; Status: not compared with conceptual translation A;Cross-references: GB:M60718; A;Accession: A36677 A; Molecule type: mRNA A; Residues: 1-728 <WEI> A; Molecule type: DNA A; Residues: 1-481, 'RT', 484-728 <SE2> A; Accession: JU0333 A; Molecule type: DNA A; Residues: 1-728 <SEK> NID:g184031; PIDN:AAA52648.1; PID:g184032 different forms of hepatocyte growth Asami, gene. O.; Hagiya fa

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A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant
A;Reference number: A39006
A;Accession: A39006
A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M5379
A;Experimental source: embryonic lung
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.;
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both
A;Reference number: PH0114; MUID:91207365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: plasma
R; Weldner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A; Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi; Reference number: A37796; MUID:91035621
; Recession: A37796; MUID:91035621
A; Molecule type: protein
A; Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X', A50-100; 1990; MUID:91035621
A; Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X', Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X', 449-450; 543-546, 'X', A10-100; MUID:90066676
A; Reference number: S06794; MUID:90066676
A; Accession: S06794; MUID:90066676
A; Accession: S06794; MUID:90066676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Note: the authors translated the codon CAG for residue 727 as Glu A:Note: part of this sequence, including the amino end of both the alpha and R:Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, F. Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A:Title: A functional domain in the heavy chain of scatter factor/hepatocyte
                                                                                                                A;Gene: GDB:HGF
A;Cross references: GDB:127524; OMIM:142409
A;Map position: 7921.1-7921.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1;
C;Complex: disulfide-bonded heterodimer of
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; R;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Hi Blochem. Blophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from A;Reference number: I52253; MUID:92062058
A;Accession: I52253
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human A;Reference number: S15443; MUID:91200041
Ccession: S15443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-288,'ET' <HAR>
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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A; Residues: 161-166
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Molecule type: mRNA
Residues: 1-288,'ET' <MIY2>
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C; Keywords: alternative splicing; yerverous; 5-1-1. The main: signal sequence #status predicted <SIG>F; 1-31. Thomain: signal sequence #status predicted <SIG>F; 32-494,495-728/Product: hepatocyte growth factor #status F; 32-494/Domain: alpha chain #status experimental <ACH>F; 118-206/Domain: kringle homology <KR1>F; 128-206/Domain: kringle homology <KR2>F; 311-288/Domain: kringle homology <KR3>F; 391-469/Domain: kringle homology <KR4>F; 391-4
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        LTYKVPQS
                                                                                                                                                                                                   NYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEICAG
                                                                                                                                                                                                                                                                                                       LKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDFVSTIDLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESPWCFTTDPNIRVGYCSQIPNCDMSHGODCYRGNGKNYMGNLSQTRSGLTCSMMDKNME
                                                                                                                                                                                                                                                                                                                                                                                      DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
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                                                          AEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHKII 720
                                                                                                                                                                    NYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEICAG
                                                                                                                                                                                                                                                                            {\tt LKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDFVSTIDLP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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No. 2
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.4e-282;
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(covalent) #status predicted
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R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R. Biochim. Biophys. Acta 1216, 299-303, 1993 A;Title: Molecular cloning and characterization of A;Reference number: $43416; MUID:94060105 A;Accession: $43416 A;Status: preliminary A;Molecula **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: S17173; M
RACCESSION: S17173
A; Molecule type: protein
A; Residues: 496-517, 'T', 519 <
R; Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBI A; Reference number: $A; Reference number: $A; A; Accession: $45521$ A; Status: preliminary A; Molecule type: mRNZ A; Residues: 1.563, 'H'A; Residues: 1.563, 'H'
A; Residues: 1-30 <RES>
A; Cross-references: EMBL: X81630; NID: g673451; PIDN C; Complex: disulfide-bonded heterodimer of chains C; Function:
A; Description: stimulates mitosis of hepatocytes a A; Description: stimulates mitosis of hepatocytes a A; Note: does not have proteinase activity C; Superfamily: hepatocyte growth factor; kringle h C; Keywords: alternative splicing; glycoprotein; gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-563,'H',565-728 <LI2>
A; Cross-references: EMBL:X72307
R; Coffer, A.; Fellows, J.; Young, S.; Pappi
Biochem. J. 278, 35-41, 1991
A; Title: Purification and characterization
R; Reference number: S17173; MUID:91354223
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A; Cros
R; Liu,
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Biochem. Biophys. Res. Commun. 199, 772-779, 1994
A; Title: Identification of mouse mammary fibroblast-derived mammary growth fancession: JC2117; MUID:94183257
A; Accession: JC2117
A; Accession: JC2117; MUID:94183257
A; Molecule type: mRNA
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 < NAT>
A; Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 < NAT>
R; Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeis
J. Biol. Chem. 270, 830-836, 1995
A; Title: Characterization of the scatter factor/hepatocyte growth and the scatter factor factor factor factor. Title: 148758; MUID:95122532
                                                                                                                                                                                                                                                                                                             A;Accession: I48758
A;Status: preliminary; translated
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Hepatocytes and sca
A;Reference number: S10966;
A;Accession: S10966
A;Status: preliminary
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A; Reference number:
A; Accession: A60185
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A; Residues: 'X',184-188, 'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,
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esidues: 496-504 <SA2>
esidues: 496-504 <L; Setter, E.; Vinter, D.W.; Osen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Co. Soc. Exp. Biol. Med. 195, 34-43, 1990; Title: Purified scatter factor stimulates epithelial; Reference number: A60185; MUID:90377927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1-563,'H',565-728
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Residues: 1-728 <LIU>
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Residues: 1-728 <SAS2>
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    does not have proteinase activity
family: hepatocyte growth factor; kringle homology; try;
rds: alternative splicing; glycoprotein; growth factor;
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er: S45521
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66; MUID:90326152
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                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDB
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RESULT A35644

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F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495,496-728/Product: hepatocyte growth factor #status
F;56-495/Domain: hepatocyte growth factor alpha chain #st.
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR2>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #st.
F;496-719/Domain: trypsin homology <KR4>
F;39/Modified site: pyrrolidone carboxylic acid (Gln) (in F;295,403,569,656/Binding site: carbohydrate (Asn) (coval)
F;488-607/Disulfide bonds: #status predicted
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Pred. No. 1e-259;
9; Mismatches 2
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A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;
F; 1-32/Domain: signal sequence #status predicted <SIG>
F; 56-495/Product: hepatocyte growth factor #status predicted <MAT>
F; 56-495/Domain: hepatocyte growth factor #status predicted <ACH
F; 129-207/Domain: kringle homology <KR1>
F; 129-207/Domain: kringle homology <KR2>
F; 310-384/Domain: kringle homology <KR3>
F; 310-384/Domain: kringle homology <KR4>
F; 410-718/Domain: kringle homology <KR4
F; 410-718/Domain: kringle 
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A;Title: Deduced primary structure of rat hepatocyte growth factor and expre A; Reference number: A35644; MUID:90222197
A;Accession: A35644
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A;Residues: 1-728 <TAS>
A;Residues: 1-728 <TAS>
A;Cross-references: GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133.1;
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hepatocyte growth factor precursor - rat N; Alternate names: hepapoietin A; scatte: C; Species: Rattus norvegicus (Norway rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Blochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte
A;Reference number: S13211; MUID:91031482
A;Accession: S13211
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;Molecule type: mRNA
;Residues: 1-728 <OKA>
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;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
;488-607/Disulfide bonds: #status predicted
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Date: 28-Sep_1990 #sequence_revision 18-Nov-1992
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                                                                                               ETTECIQGQEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS 360
                                                                                                                                                                                                                             HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL 300
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61

MWTTKCMVIFLL --

481;

Conservative

107; Pred. Score

Mismatches

20;

Gaps

5

2806; DB 1; No. 1.5e-189;

Length Indels

Similarity

68.0%; 66.1%;

TKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYE

MWVTKLLPALLLQHVLLHLLLLPIAIPYAEGQRKRRNTIHEFKKSAKTTLIKIDPALKIK 60

-----ITLAEGRGKKRNAFDDYKKTAETTLTRLNKALEVK

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A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F;42-477/Domain: hepatocyte growth factor #status predicted <AC
F;115-193/Domain: kringle homology <KR1>
F;99-275/Domain: kringle homology <KR2>
F;39-275/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR3>
F;375-453/Domain: kringle homology <KR3>
F;478-700/Domain: kringle homology <KR3>
F;478-709/Domain: kringle homology <KR4>
F;478-709/Domain: trypsin homology <KR4>
F;478-700/Domain: trypsin homology <KR4>
F;470-588/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S77422; NID:g998932; PIDN:AAB34354.1; PID:g998933 A;Note: the authors' translation for residue 458 (Thr) is inconsistent w: C;Complex: disulfide-bonded heterodimer of chains derived from the same |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Molecular cloning of Xenopus HGF cDNA and A;Reference number: I51283; MUID:95267690 A;Accession: I51283 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatocyte growth factor precursor - clawed frog N; Alternate names: hepapoletin A; scatter factor C; Species: Xenopus sp. (clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-710 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K. Mech. Dev. 49, 123-131, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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                                 (covalent) #status
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hepatocyte growth factor/scatter factor - chicken (fra
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #to
C;Accession: I51285
R;Streit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; l
Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its
A;Reference number: I51285; MUID:95237013
A;Accession: I51285
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                         A;Cross-references: GB:S77480; NID:g998675; PID:g998676
C;Superfamily: hepatocyte growth factor; kringle homolog
F;124-197/Domain: kringle homology <KRG>
F;202-279/Domain: kringle homology <KRZ>
F;296-374/Domain: kringle homology <KR3>
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A; Residues: 1-411 <STR>
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MWVTKLLPALLLQHVLLHLLLLPIAIPYAEGQRKRRNTIHEFKKSAKTTLIKIDPALKIK 60
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                                       44.18;
73.78;
                         49;
                                      Score 1821.5;
Pred. No. 1.4
                          Mismatches
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HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL
                                                                                                                                           RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTP
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                                                                       ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS
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C;Species: Homo saplens (man) . C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 C;Accession: A40331; B40331; A47135; A61395 R;Han, S.; Stuart, I. A . Docore Biochemistry 30, 9768-9780, 1991
A;Title: Characterization of the DNF15S2
A;Reference number: A40331; MUID:92002016
A;Accession: A40331 A; Accession: B40331
A; Molecule type: mRNA
A; Residues: 1-711 <HA2> A; Molecule type: DNA A; Residues: 1-711 <H A; Cross-references: <HA1> GB:M74179 locus 0p human #text_change chromosome 18-Jun-1999 ω -identification

protein

A;Cross-references: GB:M74178; NID:g183976; PIDN:AAA50165.1; PID:g183977
R;Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A;Title: Cloning, sequencing, and expression of human macrophage stimulating pr
A;Reference number: A47136; MUID:93340141
A;Accession: A47136
A;Molecule type: mRNA
A;Residues: 1-12,'C',14-622,'F',624-711 <YOS>
A;Cross-references: GB:L11924; NID:g398037; PIDN:AAA59872.1; PID:g398038
A;Cross-references: GB:L11924; NID:g398038
A;Cross-references: GB:L11924; NID:g398038
A;Cross-references: GB:L11934, 1991 partial amino acid sequence, sequen E.J.

A;Title: Macrophage stimulating protein: purification, A;Reference number: A61395; MUID:91217635 A;Accession: A61395 A; Molecule type: protein A; Residues: 230-247; 288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310, 326

source:

plasma

A;Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
A;Gene: GDB:MST1; D3F15S2; DNF15S2; HGFL
A;Cross-references: GDB:128833; OMIM:142408
A;Map position: 3p21-3p21.3
C;Complex: disulfide-bonded heterodimer of chains derived from the :
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin i
C;Keywords: duplication; glycoprotein; growth factor; kringle; plass
F;19-18/Domain: signal sequence **status predicted <SIG>
F;19-483,484-711/Product: macrophage-stimulating protein 1 *status
F;19-483/Domain: alpha chain *status predicted <ACH> plasma homology predicted precursor <MAT>

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F;191-268/Domain: kringle homology <KR2>
F;283-361/Domain: kringle homology <KR3>
F;370-448/Domain: kringle homology <KR4>
F;370-448/Domain: kringle homology <KR4>
F;484-701/Domain: beta chain #status predicted <BCH>
F;484-701/Domain: trypsin homology <TRY>
F;484-704/Domain: trypsin homology <TRY>
F;46-78,60-66,110-186,131-169,157-181,191-268,212-251,240-263,283-361,304-343,332-355,F;72,296,615/Binding site: carbohydrate (Asn) (covalent) #status predicted
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macrophage-stimulating protein 1 precursor -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan
C;Accession: JC5061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVREQSCGIKSCREAACVWCNGEEYRGAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQ
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                                                                                                                                                                                                                                                                            CLPPEWYVVPPGTKCEIAGWGETKGTGNDTVLNVALLNVISNQECNIKHRGRV--RESEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLDDNYCRNPDGSERPWCYTTDPQIEREFCDLPRCGSEAQPRQEA--TTVSCFRGKGEGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDK
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                                                                                                                                                                                                                                                                                                                                                      HMPLTGY EVWLGTLFQNPQHGEPSLQRVPVAKMVCGPSGSQLVLLKLERSVTLNQRVALI
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C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIO>
F;32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <ANT>
F;32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ANF;110-186/Domain: kringle homology <KRII>
F;191-268/Domain: kringle homology <KRII>
F;191-370/Domain: kringle homology <KRII>
F;392-370/Domain: kringle homology <KRII>
F;392-370/Domain: kringle homology <KRII>
F;392-370/Domain: kringle homology <KRII>
F;392-370/Domain: kringle homology <KRIIA-
F;392-370/Domain: kringle homology <KRIIA-
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E;489\text{-}716\text{/}Domain: macrophage-stimulating protein 1 beta chain *st $E;489\text{-}709\text{/}Domain: trypsin homology <TRY> $E;72,305,620\text{/}Binding site: carbohydrate (Asn) (covalent) *status
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X95096; NID:g1669718; PIDN:CAA64473.1; PID:g1669719 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
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A; Residues: 1-716 < OHS>
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Query Match Best Local Matches

al Similarity 315; Conserv

Conservative 118; 39.1%; 43.3%;

Score 1615; DB 1; Pred. No. 8.6e-106; Mismatches 254;

Length Indels

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Gaps

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                                                                                                                                                                         ----ISCAK----TKQLRVVNGIPTRTNIGWMVSLRYR-NKHICGGSLIKESWVLTARQC
                                                                                                                                                                                                                LKDNYCRNPDASERPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQQRNKVKASNCFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYKGTVSITKSGIKCOPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPLLLLLAQCSRALGQ----RSPLNDFQLLRGTELRNLLHPVVPGPWQEDVADAEECARRC
ESETCAGAEKIGSGPCEGDYGGPLVCEQHKMRMVLGVTVPGRGCAIPNRPGIFVRVAYYA
                                                          VSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLN
                                                                                           IWSCHDPLTGYEVWLGTINONPQPGEANLQRVSVAKTVCGPAGSQLVLLKLERPVILNHH
                                                                                                                      FPS--RDLKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDF
                                                                                                                                                      QVQFEKCGKRVDQSNRLRVVGGHP--GNSPWTVSLRNRQGQHFCGGSLVKEQWVLTARQC
                                                                                                                                                                                                                                         FWEPDA--SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPV
                                                                                                                                                                                                                                                                              SRPGLRVAFCYQIPRCTEEVVPEGCYHGSGEQYRGSVSKTRKGVQCQHW--SSETPHKPQ
                                                                                                                                                                                                                                                                                                                                        GKGEDYRGTTNTTSAGVPCQRWDAQNPHQHRFVPEKYACKDLRENFCRNPDGSEAPWCFT
                                                                                                                                                                                                                                                                                                                                                                                                                                 FDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-----TMNDTDVPLETTECIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSHPFHPEKFPDKA
                              VARICLPPEQYVVPPGTNCEIAGWGESKGTSNSTVLHVAKMKVISSQECNVKYRRRV--Q
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A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/C;Complex: disulfide-bonded heterodimer of chains derived from the same prec C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology C;Reywords: duplication; glycoprotein; growth factor; kringle c;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimen F;19-488,700main: alpha chain #status experimental <ACH>F;19-487,700main: alpha chain #status experimental <ACH>F;191-268/Domain: kringle homology <KR2>F;292-370/Domain: kringle homology <KR2>F;393-457/Domain: kringle homology <KR4>F;399-457/Domain: kringle homology <KR4>F;489-709/Domain: kringle homology <KR4>F;489-711/Tomain: beta chain #status experimental <BCH>F;480-711/Tomain: trypsin homology <KR4>F;480-711/Tomain: trypsin homology <KR4>F;481-711/Tomain: trypsin homology <KR4-F;481-711/Tomain: trypsin homol
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C; Date: 17-Jul-1992 #sequence_revision 17-Ju
C; Accession: A40332; B40332
R; Degen, S.J.F.; Stuart, L.A.; Han, S.; Jami
Blochemistry 30, 9781-9791, 1991
A; Title: Characterization of the mouse cDNA
A; Reference number: A40332; MUID:92002017
Accession: A40332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B40332
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:M74181; NID
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macrophage-stimulating protein 1 precursor - mouse N;Alternate names: hepatcoyte growth factor-like pt C;Species: Mus musculus (house mouse) C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992
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Residues: 1-716 <DEG>
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TTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMMDKNMEDLHRH
                                                                                                                           QGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESFWCF 366
                                                                                                                                                                                                                                                                                                                                                                    PEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPLLLLLVQCSRALGQRSPLNDFQLFRGTELRNLLHTAVPGP-----WQEDVADAEECARR
                                                                                                                                                                                                               DLKDNYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQRRNKGKALNCF
                                                                                                                                                                                                                                                                       GFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-----TMNDTDVPLETTECI 306
                                                                                                                                                                                                                                                                                                                                  RSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSHPFQPEKFLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSYRGTVARTAGGLPCQAWSRRFPNDHKYTPTPKNG--LEENFCRNPDGDPRGPWCYTTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESEICTEGLLAPTGACEGDYGGPLACYTHDCWVLQGLIIPNRVCARPRWPAIFTRVSVFV 706
                                                                                         RGKGEDYRGTTNTTSAGVPCQRWDAQSPHQHRFVPEKYACKDLRENFCRNPDGSEAPWCF
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A;Title: Comparison of the primary structure
A;Reference number: S03735; MUID:81212097
A;Molecnia ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmin (EC 3.4.21.7) precursor - pig (fragment)
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C;Accession: S03733; S03737; A25834
R;Schaller, J; Marti, T; Roesselet, S.J; Kaempfer, U; Rickli, E.E.
Ribrinolysis 1, 91-102, 1987
A;Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparis
A;Reference number: S03733
A;Accession: S03733
                                                                                                                                           F;1-77/Domain: plasminogen-related protein precursor homology F;1-77/Domain: activation peptide #status predicted <APT> F;7-87-560/Product: plasmin chain A #status predicted <ACH> F;84-162/Domain: kringle homology <KR1> F;84-62/Domain: kringle homology <KR2> F;86-243/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                            ns the walls of the graafian follicle; also activates A; Pathway: fibrinolysis C; Superfamily: plasmin; kringle homology; plasminoger C; Keywords: fibrinolysis; glycoprotein; hydrolase; ki F;1-790/Product: plasminogen #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eur. J. Biochem. 149, 419-400, 2000
A;Title: Determination of the complete amino-acid
A:Reference number: A25834; MUID:85203907
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F;358-435/Domain: kringle homology <KR4>
F;450-790/Product: miniplasminogen #status
F;461-540/Domain: kringle homology <KR5>
F;561-790/Product: plasmin chain B #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 450-790 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A25834;
A; Accession: A25834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-57 < BRU>
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                                                                                                                        F; 256-333/Domain:
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. Biochem. 149, 279-285, 1985
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                                                                                                                        kringle homology <KR3>
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   experimental <BCH>
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kringle; plasma; serine pr
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F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
bonds: #Status predicted
F;602,645,740/Active site: His, Asp, Ser #status predicted
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plasmin (EC 3.4.21.7) precursor - bovine
N;Alternate names: plasminogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1987 #sequence_revision 28-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YCRNPDNDEKGPWCYTTDPETRFDYCDIPEC-EDECMHCSGEHYEGKISKTMSGIECQSW
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                                                                                                                                                                               GIFVRVAYYAKWIHKII 720
                                                                                                                                                                                                                  EYLGGKVSPN--ELCAGHLAGGIDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCALPNKP
                                                                                                                                                                                                                                                     H--RGKYTLNESEICAGAEKIGSGPCEGDYGGPLVCEQHKMRMYLGVIVPGRGCAIPNRP
                                                                                                                                                                                                                                                                                                                        RPAYLDDFVSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPDGETAPWCYTTDSEVRWDYC-KIPSCGSSTTSTEHLDAPVPPEQTPVAQDCYRGNGES 365
                                                                                                                                                                                                                                                                                        SPAVITDKVIPACLPTPNYVVADRTACYITGWGETKGTYGAGLLKEARLPVIENKVCNRY
                                                                                                                                                                                                                                                                                                                                                             EWYLTAKHCLEKSSSPSSYKVILGAHEEYHLGEG---VQEIDVSKLFKEPSEADIALLKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTIVNLDHPVISCAKTK-----QLRVVNG-IPTRTNIGWMVSLRYRNK-HICGGSLIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -FDCGKPKVEPKKCPARVVGGCVSIPHSWPWQISLRYRYRGHFCGGTLISP
     #sequence_revision 28-Apr-1995 #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----NMEDL--------
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C; Function:

A; Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ns the walls of the graafian follicle; also activates the urokinase-type plasminogen status protein protein precursor homolog; plasminogen fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasminogen fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasminogen plasminogen protein precursor homology 
F; 1-26/Domain: plasminogen fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasminogen plasminogen protein precursor homology 
F; 27-103/Domain: plasminogen fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasmin status experimental <APT>
F; 104-583/Domain: activation peptide #status experimental <APT>
F; 104-583/Domain: kringle homology 
F; 104-583/Domain: kringle homology <kra>
F; 104-683/Domain: kringle homology <
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R;Berglund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Libzary, May 1994
A;Description: Cloning and characterizatin of the bovine plasminogen
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A;Residues: 706-743, 'R',745-812 <MAL>
A;Residues: 706-743, 'R',745-812 <MAL>
A;Cross-references: GB:K02935; NID:g163551; PIDN:AAA30714.1;
A;Brunlsholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-termina
A;Reference number: S03735; MUID:81212097
A;Accession: S03736
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A; Accession: I45961
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A; Residues: 27-334, D', 336-515, 'H', 517-554, 'L', 556-812
R; Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250; 1984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: liver A; Note: it is uncertain whether Met-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
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                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bonds: #status predicted F;315/Binding site: carbohydrate (Asn) (covalent) #status experimental F;315/Binding site: carbohydrate (Ser) (covalent) #status experimental F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental F;624,667,762/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-812 <BER>
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        176
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                                                                                         98
                                                                                                                                                                                                                                                  SLSRKNLAGRSVEDCAAKC--EEETDFVCRAFQYHSKEQQCVVMAENSKNTPVFRM--RD 97
                                                                                     VILYEKRIYLLECKTGNGQTYRGTTAETKSGVTCQKWSATSPHVPKFSPEKFPLAGLEEN 157
                                                                                                                                                                                                                                                                                                                                       ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 115
    YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 235
                                                                                                                                                                     FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQEN 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.1%;
35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   (%) Score 1408.5; DB 1;
(%) Pred. No. 3.3e-91;
117; Mismatches 240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasminogen. Comparison with human
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Lergier, W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812;
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YCRNPDNDENGPWCYTTDPDKRYDYCDIPEC-EDKCMHCSGENYEGKIAKTMSGRDCQAW

216

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plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiostatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: A38514; S48202; S48203
R;Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localizat A;Reference number: A38514; MUID:91184812
A;Accession: A38514
A;Molecule type: mRNA
A;Residues: 1-812 < DEG>
A;Cross-references: GB;J04766; NID:9200402; PIDN:AAA50168.1; PID:9200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Blochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076
A;Accession: S48202; MUID:95010076
   A; Accession: S48203
A; Molecule type: protein
A; Residues: 22-27 <LI2>
                                                                                   A; Molecule type: protein A; Residues: 20-25 <LIJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAVLDDFVSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHH 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVLTAAHCLDNILALSFYKVILGAHNEKVR--EQSVQEIPVSRLFREPSQADIALLKLSR 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTIVNLDHPVISCAKTK-----QLRVVNGIPTRTNI-GWMVSLRYRNKHICGGSLIKES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNYMGNLSQTRSGLTCSMW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAIITKEVIPACLPPPNYMVAARTECYITGWGETQGTFGEGLLKEAHLPVIENKVCNRNE
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F;97-581,Domain: chain A #status predicted <ACH>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <KR7>
F;582-805/Domain: trypsin homology <KR7>
F;582-805/Domain: trypsin homology <KR7>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: plasmin; kringle homology; plasminogen-related protein C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>F;1-19/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7
DTTPTIVNLDHPVIS
                                                                                                                                                                                                                                                                                                                           NYRGTVSVTVSGKTCQRWSEQTPHRHNRTPENFPCKNLEENYCRNPDGETAPWCYTTDSQ
                                                                                                                                                                                                                                                                    IRVGYCSQIPNCDMSHG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKNLKMNYCHNPDGEPRPWCFTTDPTKRWEYCDIPRCT----TPPPPPSPTYQCLKGRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGRSYKGTVSITKSGIKCOPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDPDKRYDYCNIPECEE-ECMYCSGEKYEGKISKTMSGLDCQAWDSQSPHAHGYIPAKFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1379.5;
Pred. No. 3.6e-
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acts as a
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밁 ΩV В Qγ В δÃ 밁 δÃ 망 Qy В Qy 밁

> eful in treating solid
> C; Function: C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both predictely after dissociation from the clot. In the presence of the inhibitor, the e inhibitor, the activation involves also removal of the activation peptide. C;Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiostate C; Comment: Plasminogen is synthesized by the kidney and is present in plasma and many C; Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, both plasminogen activators, both plasminogen is converted into plasmin by plasminogen activators, but plasmin angiostatin

as a proteolytic urokinase-type p plasminogen factor in

precursor home
glycoprotein;

Ş DЪ δÃ В Qy 밁 Qy

167; Gaps 22;

NRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIG 131 ILLFLLLL-----KPGQ---GDSLDGYISTQGASLFSL-----TKKQLAAGGVSDCL 50.

AKCEGE--TDFVCRSFQYHSKEQQCVIMAENSKTSSIIRM--RDVILFEKRVYLSECKTG 106

IGNGYRGTMSRTKSGVACQKWGATFPHVPNYSPSTHPNEGLEENYCRNPDNDEQGPWCYT

166

SNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYP 251 225

DKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGE 311 281

GYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFTTDPN 371

-QDCYRGNGKNYMGNLSQTRSGLTCSM 341

 ${\tt LRWEYC-EIPSCESSASPDQSDSSVPPEEQTPVVQECYQSDGQSYRGTSSTTITGKKCQS}$ PDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEG 471 400

WAAMFP--HRHSKTPENFPDAG-LEMNYCRNPDGD-KGPWCYTTDPSVRWEYCNLKRC-S 455

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N;Contains: angiostatin; microplasmin; plasminogen (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000 (C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W. J. Biol. Chem. 265, 6104-6111, 1990 A;Title: Characterization of the gene for human plasminogen, a key proenzyme A;Reference number: A35229; MUID:90202879 A;Accession: A35229;
                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:g190112;
                                                                                                                                            A; Accession: I84609
                                                                                                                                                                                                                                                                                         A; Title: Characterization of a complementary A; Reference number: I45961; MUID: 85023311
                                                                                                                                                                                                                                                                                                                                          R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W
Biochemistry 23, 4243-4250, 1984
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:X05199; NID:g35530; PIDN:CAA28831.1; PID:g35531
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Cross-references: GB:M62890; NID:g190092; PIDN:AAA36454.1; PID:g553613 Corsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O. BS Lett. 213, 254-260, 1987

A;Title: Molecular cloning and characterization of a full-length cDNA clone A;Reference number: A26646; MUID:87162490

A;Accession: A26646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:J05286; GB:M34276; NID:g190064; PIDN:AAA60113.1; A;Experimental source: leukocyte; lung fibroblast R;Malgaretti, N; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ot Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990 A;Title: Definition of the transcription initiation site of human plasmi A;Reference number: I52242; MUID:91097523
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                                                                       A; Residues:
                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                           A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                     A; Accession: I62738
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-471, 'D', 473-810 <FOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
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A; Residues: 1-810 <PET>
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<MAL3>
GB:K02921; NID:g190110; PIDN:AAA60123.1;
Lerch, P.G.; Schaller, J.; Rickli, E.E.;
                                                                                                                                                                      PIDN: AAA60124.1;
                                                                                                                                                                                                                                                                                                                   deoxyr1bonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              site of human plasminogen gene in
                                                                                                                                                                      PID: g38703
                    PID:g190111
Lergier, W.;
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                    Manneberg,
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Eur. J. Blochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain A;Reference number: A04627; MUID:77225245
A;Accession: A04627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments
A;Reference number: S03735; MUID:81212097
A;Accession: S03735
A; Molecule type: protein A; Residues: 20-50, 'Q', 51
                                                A;Reference number: A04625; MUID:75093329
A;Accession: A04625
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 20-71, 'E', 73-85, 87-106,
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A; Accession: A00929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 20-71, 'E', 73
                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 581-810 <WI1>
                                                                                                                                                          nan, B.; Wallen, P.
J. Biochem. 50, 489-494,
                                                                                                                            Structural relationship between "glutamic acid" and "lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the Atlas, Ju
ce number: A00929
51-71, 'E', 73-85, 87-100
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A; Title: Amino-acid sequence of the A; Reference number: A04626; MUID: 760 Biochem. 58, B.; Wallen, P 539-547, e of the cyanogen-bromide MUID:76043692 fragment from human plasminogen

A; Molecule type: protein
A; Residues: 483-507, 'E', 509-604 <WI3>
A; Residues: K.C.; Bernabe, P.; Arzadon, L.;
R; Robbins, K.C.; Bernabe, P.; Arzadon, L.; A; Accession: A04626 Summaria, II. The histidine loop of

J. Biol. Chem. 248, 1631-1633, 1973 A; Title: The primary structure of human plasminogen. A; Reference number: A92125; MUID:73149248 A; Contents: annotation; active site

A; Title: Studies on the active center of human A; Reference number: A92048; MUID:69234739 R; Groskopf, W.R.; Summaria, 244, ummaria, L.; Robbins, K.C. 3590-3597, 1969 plasmin. Partial amino acid sequence

R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A;Title: Structure of the omega-aminocarboxylic acid-binding sites
A;Reference number: A92382; MUID:82213905

J. Biol. Chem. 259, 13690-13694, 1984 A;Title: The fibrin-binding site of human A;Reference number: A92458; MUID:85054794 A;Contents: annotation; omega-aminocarboxylic acid binding R;Vali, Z.; Patthy, L. J. Biol. Chem. 259, 13690-13694, 1984 plasminogen. Arginines sites 32 of. and human 34 are essent plasminog

A;Contents: annotation; fibrin binding site; on R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J. J. Biol. Chem. 271, 29461-29467, J. Biol. Chem. 271, 29461-29467, Title: Kringle domains of human angiostatin. A;Reference number: A58811; MUID:97067211 A;Contents: annotation omega-aminocarboxylic acid binding site J.; Marti, D.; Soehndel, S.; McCance, S.;Characterization D.; of the anti-prolifera

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R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, Biochemistry 37, 4699-4702, 1998 A;Title: Generation of an angiostatin-like A;Reference number: A58812; MUID:9548733 fragment from plasminogen γď stromelysin-1

A.; Mulichak, A.M. annotation

submitted to the Brookhaven Protein Data Bank, A; Reference number: A51341; PDB:1PK4 July

R; Tulinsky, A.; Wu, A; Contents: annotation; X-ray crystallography, 9 angstroms, residues 376-454

A; Reference number: A51488; submitted to the Brookhaven Protein Data Bank, PDB:2PK4 July 1991

annotation; Tulinsky, A X-ray crystallography, 2.25 angstroms, residues

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ns the walls of the graaf A;Pathway: fibrinolysis C;Superfamily: plasmin; k C;Keywords: angiogenesis F;1-96/Domain: plasminoge F;1-19/Domain: signal seq
                                                                                                                                                                                                                                  A;Cross-references: GDB:11:
A;Map position: 6926-6927
A;Introns: 17/1; 62/2; 98/:
C;Function:
A;Description: dissolves tl
                                                                                                                                                                                                                                                                                                                                                                                                                    Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:THUA2) immediately af C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial cond C:Goment: Stromelysin 1 (see PIR:RCHUS1) acts on plasmin ogen to more structure of the condition of complex of human plasminog A;Reference number: A58817; MUID:94237158
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is converted by the kidney and is present in plasma and many ot C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU at PIR:FGHUGB).
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:THUA2) immediately af rg-580, resulting in two chains connected by two disulfide bonds. Without the inhibitor, C;Comment: Stromelysin is formed by autolytic cleavage of plasmin under artificial cond c;Comment: Stromelysin 1 (see PIR:RCHUS1) acts on plasminogen to produce angiostatin. To C;Genetics:
A;Gene: GDB:PLG
A;Genes: G
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A; Contents: a:
R; Padmanabhan
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A;Title: Crystal structure of the kringle 2 domain of tissue | A;Reference number: A39483; MUID: 92118803
A;Contents: annotation; X.ray crystallography, 2.4 angstroms R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A. submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65980; PDB:1KRN
A;Contents: annotation; X.ray crystallography, 1.67 angstroms R;Rejante, M.; Llinas, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: (1)H-NMR assignments and secondary structure of A; Reference number: S43645; MUID:94237157
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R.Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.

Biochemistry 30, 10589-10594, 1991

A;Title: The refined structure of the epsilon-aminocaproic acid

A;Reference number: A58818; MUID:92031503
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A;Title: Crystal and molecular structure of human eference number: A58819; MUID:92031502
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Superfamily: plasmin; kringle homology; plasminogen-related protein Kepwords: angiogenesis inhibitor; blood; duplication; fibrinolysis; il-96/Domain: plasminogen-related protein precursor homology <PLPH> 1-19/Domain: signal sequence #status predicted <SIG>
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F;20-810/Product: plasminogen #status experimental <APT F;20-96/Domain: activation peptide #status experimental <APT F;79-466/Product: angiostatin #status experimental <AST F;97-580,581-810/Product: plasmin #status experimental <CHAPT F;97-580/Domain: plasmin chain A #status experimental <CHAPT F;107-181/Domain: kringle homology <KR1>F;108-262/Domain: kringle homology <KR2>F;108-262/Domain: kringle homology <KR3>F;275-352/Domain: kringle homology <KR3>F;275-352/Domain: kringle homology <KR3>
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LNESETCAGAEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAY
                                                                                DFVSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSOHHRGKVT
                                                                                                                           EKSPRPS----SYKVILGAHQEVNL--EPHVQEIEVSRLFLEPTRKDIALLKLSSPAVIT
                                                                                                                                                                                                         FDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCL
                                                                                                                                                                                                                                     ISCAKTK-----QLRVVNGIPTRTNI-GWMVSLRYR-NKHICGGSLIKESWVLTARQCF
                                                                                                                                                                                                                                                                                            FTPETNPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAA-
                                                                                                                                                                                                                                                                                                                                   WEPDASK----LNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPV
                                                                                                                                                                                                                                                                                                                                                                            GTEASVVAPPPVVLLPNVETPSEEDCMFGNGKGYRGKRATTVTGTPCQDWAAQEPHRHSI
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                                         DKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGR
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Pred. No. 1
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F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: trypsin homology <TRY>
F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335, bonds: #status predicted
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F;622,665,760/Active site: His, Asp, Ser #status
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R;TOmlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A;Title: Rhesus monkey apolipoprotein(a). S
A;Reference number: A32869; MUID:89174660
A;Accession: B32869
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[1-96/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                       LTCSMWDKNMEDLHR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLE--TTECI 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECAAKCEEEE---EFTCRSFQYHSKEQQCVIMAENRKSSIVFRM--RDVVLFEKKVYLSEC
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ilarity 33.8%; Pred. No. 2e-88;
Conservative 127; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Lawn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, J. Biol. Chem. 270, 24004-24009, 1995
A;Title: The recurring evolution of Lp(a): Insights from cloning A; Reference number: I46259; MUID:96025778
A; Accession: I46260
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Plasmin (EC 3.4.21.7) precursor - western European hedgehog plasmin (EC 3.4.21.7) precursor - western European hedgehog C;Species: Erinaceus europaeus (western European hedgehog) C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_chr
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                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                              F:379-456/Domain: kringle
F:482-561/Domain: kringle
F:582-803/Domain: trypsin
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A; Residues: 1-810 <LAW>
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Best Local Similarity
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    298
                                            212
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                                                                                                                                                                                                                 118 LYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                742
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                                                                                                                                                                                                                                                                                           TKK---VNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFD
                                      QIPHPHGFIPSKFPSKNLKMNYCRNPDGEPRPWCFTMDRNKRWEYCDIPRCT----TP
                                                            QTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTD 297
                                                                                                                                    RNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDH 237
VPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCR 355
                                                                                                                RNPDNDPKGPWCYTMDPEVRYEYCETIQC-EDECMHCSGQNYVGKISRTMSGLECQPWDS 211
                                                                                                                                                                                          LFEKKMYLSECKVGNGKYYRGTVSKTKTGLTCQKWSAETPHKPRFSPDENPSEGLDQNYC
                                                                                                                                                                                                                                                                     TKKQLSVGSTEECAVKC--EKETSFICRSFQYHSKEQQCVIMAENSKSTPVLRM--RDVI 92
                                                                                                                                                                                                                                                                                                                                                     277;
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                                                                                                                                                                                                                                                                                                                                                   Conservative 110;
                                                                                                                                                                                                                                                                                                                                               32.8%; Score 1353.5;
35.1%; Pred. No. 2.40
tive 110; Mismatches
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2.4e-87;
hes 255;
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A; Status, F.Z.-A; Molecule type: DNA
A; Residues: 1-16 < RES>
A; Cross-references: GB:L07899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:X06290; EMBL:X06696; NID:g28619; PIDN:CAA29618.1; PID:g28620 R;Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987 A;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologou A;Reference number: A28017; MUID:87204109 A;Accession: A28017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen A; Reference number: $00657; MUID: $8039109 A; Accession: $00657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
N.Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
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A;Accession: A47277
                                                                                                                                                                                                                                                                                            X',4396-4401 <EAT>
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.;
Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A;Title: 5' control regions of the apolipoprotein(a) of
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 20-21,'P',23-34;177-179,'N',181-186,'T',188-196,'DKG',200;292-314,'W',316-3
X',4396-4401 <EAT>
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A; Residues: 1-4548 < MCL>
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                                                                                                                                                            A; Status: preliminary; translation not shown; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTPTIVNLDHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRVRNKHICGGSLIKESWVLTA 532
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    NID:g967973; PID:g967974 Magnaghi, P.; Bruno, L.;
        Ľ.;
                                                                                                                                                                                                                                                                                                                                                                  Zysow,
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        Pontoglio,
                                                                                                                                                                    from
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                                                                                                                                                                GB/EMBL/DDB
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        M.; Rocchi,
                                                                                                                                                                                                                                                                                                                                                                  Meer, K.;
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F:1282-1359/Domain: kringle he F:1396-1473/Domain: kringle he F:1510-1587/Domain: kringle he F:1624-1701/Domain: kringle he F:1624-1701/Domain: kringle he F:1638-1815/Domain: kringle he F:1852-1929/Domain: kringle he F:1966-2043/Domain: kringle he
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;20-4548/Product: apolipoprotein(a) #status
F;28-105/Domain: kringle homology <KR1>
F;142-219/Domain: kringle homology <KR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: apolipoprotein(a); kringle homology; trypsin C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M90078; NID:g178786; PIDN:AAA35547.1; A;Note: apo(a) gene 1 (nomenclature of reference I52415) A;Accession: A47233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning
A;Reference number: A47233; MUID:93087573
A;Accession: I60906
                                                                            F;3106-3183/Domain:
F;3220-3297/Domain:
                                                                                                                                                                                                                          F;2308-2385/Domain:
F;2422-2499/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1054-1131/Domain: kringle F;1168-1245/Domain: kringle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: several genes rs of kringle repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-16 < RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Multiple members of the plasminogen-apolipoprotein(a) A;Reference number: I52415; MUID:92207924 A;Accession: I52415
                     F;3562-3639/Domain:
                                        F; 3448-3525/Domain:
                                                             F; 3334-3411/Domain:
                                                                                                                      F; 2992-3069/Domain:
                                                                                                                                            F; 2878-2955/Domain:
                                                                                                                                                                                F; 2650-2727/Domain:
                                                                                                                                                                                                       F; 2536-2613/Domain:
                                                                                                                                                                                                                                                                 F;2194-2271/Domain:
                                                                                                                                                                                                                                                                                      F; 2080-2157/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120699; OMIM:152200 A;Map position: 6q26-6q27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M86877; NID:g178780; PIDN:AAB49909.1; A;Note: apo(a) gene 1 (nomenclature of reference I52415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 31,
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A; Residues: 1-16 < RE5>
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MEDILIBE-9936858; Pubmed-9817840;

Ultsch M., Lokker N.A., Godowski P.J., de Vos A.M.;

"Crystal structure of the NKI fragment of human hepatocyte growth factor at 2.0-A resolution.";

"Structure 6:1383-1393(1998).";

L Structure 6:1383-1393(1998).

C -!- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND AC C. AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYP IT HAS NO DETECTABLE PROTEASE ACTIVITY.

C -!- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A DISULFIDE BOND.

C -!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.

C -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                the European Bioinformatics Institute.
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or send an email to license@isb-sib.ch).
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MEDILINE-98154323; PubMed-9493772;

Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,

Rubin J.S., Bottaro D.P., Byrd R.A.;

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factor reveals a potential heparin-binding site.";
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Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
Baker J.B., Godowski P.J.;
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Identification of variants that lack mitogenic activity yet retain
high affinity receptor binding.";
EMBO J. 11:2503-2510(1992).
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Nakamura T., Shimizu
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"Structural organization and the transcription human hepatocyte growth factor gene.";
Biochemistry 30:9170-9176(1991).
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on the alpha chain.";
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H., Gohda E., Kitamura
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Growth factor; Kringle; Glycomercials
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                                                                                                                                     Hepatocyte growth (Hepatopoeitin A).
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Pred. No. 6.5
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Sciurognathi;
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(Scatter fa
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chi; Muridae;
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; Murinae; Mus
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EMBL; X72307; CAA51054.1; ALT_INIT.
HSSP; P14210; 1BHT.
MGD; MGI:96079; Hgf.
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR0003014; PAN.
InterPro; IPR003609; Pan.app.
InterPro; IPR001254; Trypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                   Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00718; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00070; KRINGLE_1; 4.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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or send a
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Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin;
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Biochim. Biophys. Acta 1216:299-303(1993).

-!- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL
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Sasaki M., Nishio M., Sasaki T., Enami J.;
Sasaki T., Enami J.;
"Identification of mouse mammary fibroblast-derived
factor as hepatocyte growth factor.";
                                              CHAIN
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Lee C.C., Kozak C.
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.A., Yamada K.M.
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HGF_RAT
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01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Hepatocyte growth factor precursor (Scatter factor)
(Hepatopoeitin A).
                                                                                                                                                                                                                                                                                          PIR; S13211; S13211.
PIR; A35644; A35644.
HSSP; P14210; 1BHT.
MEROPS; S01.978; -.
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P17945;
01-NOV-1990
                                                                                                                                                              InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; pan.
InterPro; IPR003018; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; kringle; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Deduced primary structure of rat hepatocyte growth expression of the mRNA in rat tissues."; Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                   PRINTS; PR00722; CHYMOTRY PRINTS; PR00018; KRINGLE.
                                                                                                      Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90102; BAA14133.1; EMBL; X54400; CAA38266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
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Okajima A., Miyazawa K., Kitamura N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Toshiro K., Hagiya M.,
Shimizu S., Nakamura T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-WISTAR;
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Mammalia; Eutheria; Rodentia;
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SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY.
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATCOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, A AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELLIT HAS NO DETECTABLE PROTEASE ACTIVITY.

SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
; SM00130; KR; 4.
; SM00473; PAN_AP; 1.
; SM00020; Tryp_SPc; 1.
TE; PS00021; KRINGLE_1; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y structure of rat hepatocyte growth factor A during liver regeneration following hepati Biochem. 193:375-381(1990).
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LPSYGCTIPEKTTCSIYGWGYTGLINADGLLRVAHLYIMGNEKCSQHHQGKVTLNESELC
        LPNYGCTIPEKTSCSYYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEIC
                                                                      DHPVISCAKTKQLRVVNGIPTQTTVGWMVSLKYRNKHICGGSLIKESWVLTARQCFPARN
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PAP.

KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.

BY SIMILARITY.

BY SIMILARITY.
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Pred. No. 1.1e-276;
Nismatches 27;
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N-LINKED (GLCNAC. . .) (POTENTIAL).

3E0BF1F96ADCEDFF CRC64;
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HEPATOCYTE GROWTH FACTO
PYRROLIDONE CARBOXYLIC
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RESULT HERE ELECTION AND ELECTI
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YOShimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
YOShimura T. Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
TCloning, sequencing, and expression of human macrophage stimulating protein (MSP, MST1) confirms MSP as a member of the family of kringle proteins and locates the MSP gene on chromosome 3.";
J. Biol. Chem. 268:15461-15468(1993).
1- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACTIVITY, SINCE CRUCIAL ANCHERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGFL_HUMAN STANDARD; PRT; 711 AA.
P26927; Q13350; Q14870;
Q1-AUG-1992 (Rel. 23, Created)
O1-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP) (Macrophage stimulating protein)
MST1 OR HGFL.
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MSTI OR HGFL.
Homo sapiens (Human).
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Biochemistry 30:9768-9780(1991).
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NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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locus on human chromosome 3:
ביי לחוד kringle domains with
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EMBL; M74178; AAA50165.1; -.
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HSSP; P00747; 2PK4.
MEROPS; S01.975; -.
MIM; 142408; -. Pfam; Pfam; InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR0030014; PAN.
InterPro; IPR00309; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 4. use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See tities requires a license agreement (See http://www.isb-sib.send an email to license@isb-sib.ch). PF00051; PF00024; PF00089; kringle; PAN; 1. trypsin; Usage bу and for

CHYMOTRYPSIN. KRINGLE.

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PROSITE: PS50070; KRINGLE_2;
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C -> F.
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L -> F (IN REF. 2)
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Hepatocyte growth f
                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-92002017; PubMed=1832957;
Filezner Degen S.J., Stuart L.A., Han S., Jam "Characterization of the mouse cDNA and gene growth factor-like protein: expression during Biochemistry 30:9781-9791(1991).

-i- FUNCTION: PROBABLY HAS NO PROTEOLYTIC ACT CHARACTERISTIC OF SERINE PROTEASES CATALY
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                                                                                 POLYPEPTIDES.
SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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PTM: MAY BE CLEAVED AFTER !
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Pyright. It is produced through a collaboration e of Bioinformatics and the EMBL outstation .
Institute. There are no received.
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DE BONDS,
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Sciurognathi; Muridae;
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PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
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HSSP;
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SMART; SM00020; Tryp_SPc; 1.
SPROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
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srPro; IPR001314; Chymotrypsin.
srPro; IPR000001; Kringle.
srPro; IPR003014; PAN.
srPro; IPR003609; Pan.app.
srPro; IPR001254; Trypsin.
n; PF00051; Kringle; 4.
n; PF00024; PAN; 1.
CTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:96080;
                                  LPLLLLLVQCSRALGPRSPLNDFQLFRGTELRNLLHTAVPGP----WQEDVADAEECARR
                                                        LHLLLPIAIPYAEGORKRRNTIHEFKKSAKTTLIKI---DPALKIKTKKVNTADOCANR
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KRINGLE 3.
KRINGLE 4.
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POTENTIAL.
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nes 263;
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Schaller J., Marti T.,
Schaller J., Marti T.,
"Amino acid sequence c
of the carbohydrate at
species.";
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miniplasminogen."
Eur. J. Biochem.
                                                      MEDLINE-85203907; Repair Marti T., Schaller
                                                                                                                                 Fibrinolysis 1:91-102(1987).
                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig).
                                    "Determination of the complete amino-acid
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1 (Rel. 40, Last:
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Matches

294;

Conservative

114; Pred.

36.98;

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Best Local Similarity

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CCCCCCCCCCRATRA RANGE
Query Match
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InterPro; IPRO0001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
Pfam; PF00051; Kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00029; trypsin; 1.
Pfam; PF00029; trypsin; 1.
Pfam; PF00029; trypsin; 1.
Pfam; PF00018; KRINGLE.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 5.
SMART; SM00130; KR; 5.
SMART; SM00120; TRYP_SPC; 1.
SMART; SM00020; Tryp_SC; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS00070; KRINGLE_2; 5.
PROSITE; PS00070; KRINGLE_2; 5.
PROSITE; PS00070; KRINGLE_2; 5.
PROSITE; PS00070; KRINGLE_2; 5.
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-I. FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTECLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, THOOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND VON WILLEBRAND FACTOR.

-I. ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

-I. PTM: N-LINKED GLYCAN CONTAINS N-ACETYLLACTOSAMINE, SIALIC ACID AND IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).

-I. MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

-I. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TENDORYN EMMITY DIA SUMMACHINE SITERAMITY
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ACT_SITE
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PROSITE; PS50070; KRINGLE_2; 5
PROSITE; PS50240; TRYPSIN_DOM;
PROSITE; PS00134; TRYPSIN_HIS;
PROSITE; PS00135; TRYPSIN_SER;
                                                                             SEQUENCE
                                                                                                                               CARBOHYD
                                                                                                                                                                               CARBOHYD
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PIR; S03733; S03733.
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MEDLINE=88185329; PubMed=3356193;
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CARBOHYDRATE-LINKAGE
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N-LINKED (GLCNAC. .).
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O-LINKED (GALNAC. .).
/FTTIG=CAB_000020. .).
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KRINGLE
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F04EA06E74BCD58E CRC64;
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Bovinae; Bos
             Eutheria;
                       (Bovine).
Metazoa;
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      Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen. Species specificity in relation to sialylation and fucosylation patterns.";
Eur. J. Biochem. 173:57-63(1988).
-i- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
                                                                         InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                          PIR; A25835; PLBO.
HSSP; P00747; 2PK4
MEROPS; S01.233;
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Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
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Biochemistry 23:4243-4250(1984).
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Marti T., Schaller J., Rickli E.E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O-LINKED GLYCANS CONSIST OF GAL-GALNAC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY). MISCELLANBOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT. SIMILARITY: CONTAINS 5 KRINGLE DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMININ AND VON WILLEBRAND FACTOR.
ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINGGEN
ROTIVATORS, BOTH PLASMINGEN AND ITS ACTIVATOR BEING BOUND TO
FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
PTM: N-LINKED GLYCAN CONTAIN N-ACETYLLACTOSAMINE AND SIALIC ACID.
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AND INFLAMMATION; IN OVULATION IT WEAKENS THE WALLS OF THE
GRAAFIAN FOLLICLE. IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
INMITTA NOT CON COLTEGERORS.
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                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                      2PK4.
                                               kringle;
trypsin; 1
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PubMed=6148961;
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                                                  Trypsin.
;le; 5.
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E3
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bovine plasminogen cDNA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
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Best Local Sin
Matches 280;
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PROSITE; PS00021; KRINGLE_1; 5.

PROSITE; PS50070; KRINGLE_2; 5.

PROSITE; PS50240; TRYPSIN_DOM; 1

PROSITE; PS00134; TRYPSIN_HIS; 1

PROSITE; PS00135; TRYPSIN_SER; 1
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SMART;
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                                                                                                                                                                                                                                                                                                 56 ALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHE 115
                                                                                                                                                                                                                                  VILYEKRIYLLECKTGNGQTYRGTTAETKSGVTCQKWSATSPHVPKFSPEKFPLAGLEEN
                                                                                   CRNPDGSESPWCFTTDPNIRVGYCSQIPNCDMSH--
                                                                                                                  TDVPLE--TTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENY
                                                                                                                                                DSQSPHAHGYIPSKFPNKNLKMNYCRNPDGEPRPWCFTTDPQKRWEFCDIPRCT-----
                                                                                                                                                            DHQTPHRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMND
                                                                                                                                                                                          YCRNPDNDENGPWCYTTDPDKRYDYCDIPEC-EDKCMHCSGENYEGKIAKTMSGRDCQAW
                                                                                                                                                                                                   YCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRW 235
                                                                                                                                                                                                                                                      FDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQEN 175
                                                                                                                                                                                                                                                                          SISRKNLAGRSVEDCAAKC--EEETDFVCRAFQYHSKEQQCVVMAENSKNTPVFRM--RD
                                          KNYMGNLSQTRSGLTCSMW------
                                                               CRNPNGEKAPWCYTTNSEVRWEYCT-IPSCESSPLSTERMDVPVPPEQTPVPQDCYHGNG
                                                                                                         TPPPSSGPKYQCLKGTGKNYGGTVAVTESGHTCQRWSEQTPHKHNRTPENFPCKNLEENY
                      QSYRGTSSTTITGRKCQSWSSMTPHRHLKTPENYPNAGLTMNYCRNPDADKSPWCYTTDP
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SM00473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        remodeling;
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PR00018;
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35.4%;
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N -> D (IN REF. 2).
Q -> H (IN REF. 2).
P -> L (IN REF. 3).
T -> R (IN REF. 3).
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/FTId=CAR_000015.
/ETId=CAR_000015.
CHARGE RELAY SYSTI
CHARGE RELAY SYSTI
                                                                                                                                                                                                                                                                                                                              Score 1408.5; DB Pred. No. 9.6e-98;
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KRINGLE
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LIGHT CHAIN
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                                                                                                                                                                                                                                                                                                                     240;
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                                                                                    -GQDCYRGNG
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RVRWEECNLKKCSETPEQVPAAPQAPGVENPPEADCMIGTGKSYRGKKATTVAGVPCQEW

509

-MEDLHRHIFWEPDA---SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTT

В

way

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"Anglostatin: a novel anglogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma."; Cell 79:315-328(1994).

-i- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, AND INFLAMMATION; IN OVULATION IT WEAKERS THE WALLS OF THE GRARFIAN FOLLICLE. IT ACTIVATES THE UROXINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND YOU WILLEBRAND FACTOR.
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01-FEB-1991
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Degen S.J., Bell S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O'Reilly M.S., Holmgren L., Shing Y., C
Moses M., Lane W.S., Cao Y., Sage E.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF ANGIOSTATIN, AND MEDLINE-95042728; PubMed-7525077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Degen S.J., Bell S.M., Schaefer L.A., 
"Characterization of the cDNA coding 
localization of the gene to mouse characterization of the gene to mouse characterists 
Genomics 8:49-61(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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      ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.

MISCELLANDOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.

MISCELLANDOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELL TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.

SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
                                                                                                                                                                                                                                 FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND
                                                                                                                                                                                                                METASTATIC TUMORS IN VIVO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRVAYYAKWIHK 718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQEPHQHSIFTPETNPQSGLERNYCRNPDGDVNGPWCYTMNPRKPFDYCDVPQCESS--
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1 (Rel. 17, Last sequent (Rel. 40, Last annotation)
2 precursor (EC 3.4.2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2081600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
(EC 3.4.21.7) [Contains: Anglostatin].
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PROSITE; PS50070; KRINGLE_2; 5.

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MGD; MGI:97620; PJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Experimental Bioinformatics Institute. There are no restaurable to the swiss of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS TRYPSIN FAMILY. PLASMINGEN SUBFAMILY.
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"Characterization of a complementary";
"Studies on the active center of human plasm sequence of a peptide containing the active J. Biol. Chem. 244:3590-3597(1969).
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MEDLINE=75093329; I
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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.3e-95;
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and distance geometry.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schaller
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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   SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr:
13: sp_vertebr:
14: sp_unclass
15: sp_bacteri
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17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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4126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fungi:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
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sp_mammal:*
sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15 16	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result No.
1371 1365	1388.5	1401.5	1452	1579	1605	1615	1624	1627	1632	1652.5	1704	2806	3170	3880	Score
33.2 33.1	33.7	34.0	35.2	38.3	38.9	39.1	39.4	39.4	39.6	40.1	41.3	68.0	76.8	94.0	Query Match I
810 567	812	812	806	709	716	716	296	704	290	717	716	710	726	728	Query Match Length DB
4 Q15146 4 Q13208	11 Q91WJ5	11 Q9R0	6 01878	13 Q90ZN6	11 Q91X	11 P70521	4 01451	13 Q908	4 00293	13 P70006	13 Q916	13 09140	13 Q90978	6 Q9вн09	B ID
ω σ.	75	¥3	ω	N6	38	21	v	55	G 1	96	91	22	78		; ; ; ;
Q15146 homo sapien Q13208 homo sapien	Q91wj5 mus musculu	Q9r0w3 rattus norv	018783 macropus eu	Q90zn6 brachydanio	Q91xg8 mus musculu	P70521 rattus norv	Q14519 homo sapien	Q90865 gallus gall	Q02935 homo sapien	Ų١	Q91691 xenopus lae	Q91402 xenopus. he	Q90978 gallus gall	Q9bh09 felis silve	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
338	338.5	340.5	344.5	354	365	393	402	423.5	435	435.5	439	462	471	494.5	500	523.5	549.5	555.5	556.5	615	654.5	785	945	1036	1040	1139	1139	1364.5
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275	329	643	389	339	273	431	395	560	265	385	75	616	597	608	607	516	559	286	334	109	313	454	2869	211	215	210	208	648
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Q96RZ6	042272	097506	Q9PVX7	Q99L44	Q921N4	Q969W6	Q9BZW1	Q14520	Q90WS3	Q25101	Q9BGN9	097507	035727	Q9PTW7	Q91001	Q9BU99	Q91VP2	Q13209	046507	Q9N1B8	Q9PU78	046506	Q28398	055027	042341	Q13494	Q9BYM0	Q9H1V4
Q96rz6 homo sapien	O42272 xenopus lae	S	Q9pvx7 xenopus lae	Q99144 mus musculu	mus	Q969w6 homo sapien		Q14520 homo sapien	Q90ws3 elaphe sp.	Q25101 herdmania m	sod	ເດ	O35727 mus musculu		\rightarrow	homo	Q91vp2 mus musculu				m	046506 papio hamad	Q28398 erinaceus e		1 gall	Q13494 homo sapien	Q9bym0 homo sapien	Q9h1v4 homo sapien

ALIGNMENTS

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Hydrolase; SEQUENCE

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functions

59 61

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Q90978 PRELIMINARY; PRT; 726 AA.
Q90978; Q90866;
01-JAN-1998 (TEMBLrel. 05, Created)
01-JAN-1998 (TEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR / SCATTER FACTOR PRECURSOR.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                 HILTYKVPQS
                                                                                                                                                                                                                                                                                                                     LPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEIC
                                                                                                                                                                                                                                                        AGAENTVSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHK
                                                                                                                                                                                                                                                                     AGAEKIGSGPCEGDYGGPLVCEQHKMRMYLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHK 718
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                                                                                                                                                                                                                                                                                                                                                                                                                          DLHRHIFWEPDASKLNKNYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRHKFLPERYPDKGFDDNYCRNPDGKPRPWCYTLDPDTPWEYCAIKMCAHSTMNDTDVPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NKDYIRNCIIGKGRSYKGTVSITKSGIKCOPWSSMIPHEHSFLPSSYRGKDLQENYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGPWDHTESGKICQRWDRQTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKDYIRNCIIGKGGSYKGTVSITKSGIKCQPWNSMIPHEHSFLPSSYRGKDLQENYCRNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKKVNTADQCANRCTRNKGLPETCKAFVEDKARKQCLWFPENSMSSGVKKEFGHEFDLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MWVTKLLPALLLQHVLLHLLLLPIAIPYAEGQRKRRNTIHEFKKSAKTTLIKIDPALKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MWVTKLLPVLLLQHVLLHLLLLP--IPYAEGQKKRRNTLHEEKKSAKTTLIKEDPLLKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease.
728 AA; 83067 MW;
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Pred. No. 0;
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                                    Phasianinae;
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Best Local
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pfam; pr00024; paN; 1.

pfam; pr00028; trypsin; 1

pfam; pr00089; trypsin; 1

prinvs; pr00022; cifwortrypsin.

prinvs; pr00020; kringle

smarr; sm00130; kr; 4

smarr; sm00130; kr; 4

smarr; sm0020; tryp_spc; 1.

smarr; sm00020; tryp_spc; 1.

pr0site; ps00071; kringle 1; 4

pr0site; ps50070; kringle 2; 4

pr0site; ps50240; trypsin_dow; 1.

alternative splicing; Glycoprotein;

scripe receased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95237013; PubMed=7720585;
Streit A., Stern C.D., Thery C., Ireland
Sharpe M.J., Gherardi E.,
"A role for HGF/SF in neural induction ar
node during gastrulation.";
Development 121:813-824(1995).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMI
TRYPSIN FAMILY.
                             301
                                                                                                                                                                                                                                                                                                                                                                          SIGNAL CHAIN SEQUENCE
                                                                                                         177
                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Glycoprotein; Growth factor; Serine protease; Serine protease homolog; Signal. SIGNAL 1 27 POTENTIAL.
                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001311; Chymotrypsin.
InterPro; IPR003011; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003509; Pan_app.
InterPro; IPR001254; Trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thery C., Sharpe M.J., Batley S.J. "Expression of HGF/SF, HGFI/MSP, during early chick development.",
Dev. Genet. 17:90-101(1995).
                                                                                                                                                                                                                                                              1 MWVTKLLPALLLQHVLLHLLLLPIAIPYAEGQRKRRNTIHEBKKSAKTTLIKIDPALKIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WHITE LEGHORN, AND RHODE ISLAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96029010; PubMed=7554499; Thery C., Sharpe M.J., Batley S.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDWTPENFKCKDLRENYCRNPDGS
                                                                                        HKHKFRPERYPDKGFDDNYCRNPDGKLRPWCYTLDPNTPWEFCAIKTCDVGTLNSTEAVA
                                                      HRHKELPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL
                                                                                                                                            KKDYVRNCIIGKGAEVKGTISITKSGTQCQAWNSMIPHEHSFLPSSYRGKDLRENYCRNP
                                                                                                                                                          NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP
                                                                                                                                                                                             TKLLNTTEQCAKRCSRNKGLSETCKAFAYDRVTKRCHWLSFNSLTNGVRKKQDHAFDLFE
                                                                                                                                                                                                            TKKVNTADQCANRCTRNKGLPETCKAEVEDKARKQCLWEPENGNSSGVKKEEGHEEDLYE
                                                                                                                                                                                                                                               MWATQLLPALLLH----QLLLPPITIPAAEGKGKRRNPLHDYKKTGELMLIKVNKTLEVK
                                                                                                                                                                                                                                                                                                             544;
                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                          726 AA;
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                      726
; 82913
                                                                                                                                                                                                                                                                                                                     76.8%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                       MW;
                                                                                                                                                                                                                                                                                                        92;
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Pred.
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; 5805F048A5766C38 CRC64;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                    3170;
No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ireland
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l.4e-280;
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SCATTER

FACTOR

Kringle;

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Gaps

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361 297

ETTTCIQGQGEGYRGTVNTIWSGIQCQRWDSQFPHQHNITPENFKCKDLRENYCRNPDGS

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  Pfam; PF00051; kringle; 4.
Pfam; PF00084; PAN; 1.
Pfam; PF00089; trypsin; 1.
PFAm; PF00089; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
SMART; SW00130; KR; 44.
SMART; SW00130; KR; 47.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS00021; KRINGLE_1; 3.
PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           091402;
01-NOV-1996
01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                         Nakamura H., Tashiro K., Nakamura T., 
"Molecular cloning of Xenopus HGF cDN 
Xenopus early embryogenesis."; 
Mech. Dev. 49:123-131(1995).
                                                                                                                                                                                                                                                                                                                                                           Mech. Dev. 40....
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
TISSUE=TAILBUD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopodinae.
NCBI_TaxID=8353;
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Amphibia; Batrachia;
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                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95267690; PubMed=7748783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus
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                                                                                                                                                                                                                                                                                                                  S77422; AAB34354.2;
P14210; 1BHT.
SM00130; KR; 4.
SM00473; PAN_BP; 1.
SM00020; Tryp_SPc; 1.
; PS00021; KRINGLE_1;
; PS50070; KRINGLE_2;
                                                                                                                                                                                                                     IPR001314; Chymotrypsin.
IPR000001; Kringle.
IPR003014; PAN.
IPR003609; Pan_app.
                                                                                                                                                                                                  IPR001254;
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                                                                                                                                                                                                Trypsin
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Mesobatrachia; Pipoidea;
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Q91691 PRELIMINARY; PRT; 716 A
Q91691;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence
01-DEC-2001 (TrEMBLrel. 19, Last annotatic
GROWTH FACTOR LIVERTINE.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50240; TRYPSIN_DOM;
Hydrolase; Serine protease.
SEQUENCE 710 AA; 81487 MW;
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                                                                                                                               IILTYKVP 726
                                                                                                                                                                                                                                                                                      DLKRHTFNEPDVSILQKNYCRNPDNDAHGPWCYTDDPFVPWDYCPISRCEGDTAKIMANI
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66.1%;
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                                  Last sequence up
Mesobatrachia; Vertebrata; I
Mesobatrachia; Pipoidea;
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Pred. No. 2.4e-247;
7; Mismatches 120;
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          Euteleostomi;
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R Pfam; PF000524; PAN; 1.

R Pfam; PF000024; PAN; 1.

R Pfam; PF000089; trypsin; 1.

R PRINTS; PR00018; KRINGLE.

R SMART; SM00130; KR; 4.

R SMART; SM00020; Tryp_SPc; 1.

R SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 4.

PROSITE; PS00021; KRINGLE_2; 4.

PROSITE; PS50070; KRINGLE_2; 4.

PROSITE; PS50070; TRYPSIN_DOM; 1.

W Hydrolase; Serine protease.

O SEQUENCE 716 AA; 81971 MW; 508376A0E4398798 CRC64;
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Best Local Similarity
                                                                                                                                                                           440
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
EMBL: U57455; AAB52574.1; -.
HSSP; P00747; 1CEA.
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InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
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NCBI_TaxID=8355;
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DGLLRVAHLYIMGNEKCSOHHRG-KVTLNESEICAGAEKIGSGPCEGDYGGPLVCEOHKM
                                              PINKIVCGPSDSSLVMLKLERPITLNSRVALICLPPERYIVPEETKCEIAGWGDTRGTGH
                                                                 NVSQLVYGPEGSDLVLMKLARPAVLDDFVSTIDLPNYGCTIPEKTSCSVYGWGYTGLINY
                                                                                                       VSLRNRQGEHFCGGSLVKENWVISTRQCFSSCDADLSGYEAVMGTLFKNPSPDDPDKQSV
                                                                                                                          VSLRYR-NKHICGGSLIKESWVLTARQCFPS--RDLKDYEAWLGIHDVHGRGDEKCKQVL
                                                                                                                                                                  MDPNTPFDYCAIKPCEGEKVLTLEEAESIVFDSCGKRNDRIFQKSRIVGGVP--GNSPWT
                                                                                                                                                                                              GNPLIPWDYCPISRCEGDTTPTIVNLDHPVI-SCAKT----KQLRVVNGIPTRTNIGWM
                                                                                                                                                                                                                           NGELYSGRVSKTRKGIKCRRWEEKRNDLELSLD-QPYLVPLEENYCRNPDRDSHGPWCYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.3%; Score 1704; DB 13;
44.5%; Pred. No. 9.8e-147;
Live 124; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00051; kringle; 4.

Pfam; PF00024; PAN; 1.

Pfam; PF000089; trypsin; 1.

Pfam; PF000089; KRINGLE.

SMART; SM00130; KR; 4.

SMART; SM00130; KR; 4.

SMART; SM00200; Tryp_SPc; 1.

PROSITE; PS00021; KRINGLE_1; 3.

PROSITE; PS00070; KRINGLE_2; 4.

PROSITE; PS50070; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aberger F., Schmidt G., Richter K.;
"The Xenopus homologue of hepatocyte growth factor-like protein specifically expressed in the presumptive neural plate American gastrulation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                  257
                                                                   186
                                                                                                                197
                                                                                                                                                                 128
                                                                                                                                                                                                                137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000001;
InterPro; IPR003014;
InterPro; IPR003609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mech. Dev. 54:23-37(1996).
EMBL; Y08734; CAA69989.1; -
HSSP; P00747; ICEA.
MEROPS; S01.977; -
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355;
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DNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLETTECIQGQGEGYRGT
                                                                                                                                                                           KGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGDWCFTSNPEV
                                                                                                                                                                                                                                                                                                                                                                               LHLLLLDTAIPYAEGQRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTR
                                                 RHQYCGIKKCEDAVCLTCNGEDYRGSVDRTESGKECQRWDLQAPHTHPYKPEKYPDKSLD
                                                                                   RYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTDHRHKFLPERYPDKGFD
                                                                                                                                                 RGTVSKTKNGRTCQHWRLKFPHDHKFSDTHW--PELEENYCRNPDSDPEGLWCYTTDKNI
                                                                                                                                                                                                                                               ----LLDCRSFDYNWKSQSCRLLPWTQNSSNVLLQRNVQYDLYQKKDYIRDCVVGNGNTY
                                                                                                                                                                                                                                                                                              NKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSY
                                                                                                                                                                                                                                                                                                                                                LFLLCFNAAVFFVTG-TAHRSALNDYQRSKGLELVHMNEG-GVKQEVQAEIQICAKQCSD
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717 -
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717 H
82017 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.1%; Score 1652.5; DB 13;
42.8%; Pred. No. 4.9e-142;
tive 126; Mismatches 258; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAN.
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RESULT
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                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-93087571; PubMed=1280830;

Hartmann G., Naldini L., Weidner K.M., Sachs M., Vigna Comoglio P.M., Birdmeier W.;

"A functional domain in the heavy chain of scatter face of the control of th
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Q02935;
                                           -!- SIMILARITY: CONTAINS TWO KR
-!- SIMILARITY: HIGH, TO OTHER
EMBL; X57574; CAA40802.1; -.
EMBL; L02931; AAA52649.1; -.
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
HEPATOCYTE GROWTH FACTOR, HEAVY CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor gene.";
Eur. J. Biochem. 197:15-22(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Miyazawa K., Kitamura A., Naka D.,
"An ulternatively processed mRNA go
growth factor gene.":
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91200041; PubMed=1826653;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMGTLFKNPSPDDPDRQSVPISKIVCGPSDSSLVMLKLQWPVTLNSRVALICLPPERYIV
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                                                                                                                                                                   NO DETECTABLE PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Kringle.
                                                                                                                   TWO KRINGLE REGIONS.
OTHER HGF; LOWER, TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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AND CELL
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TYPES. IT
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29 RESULT 10 RES
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Best Local
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Pfam; PF00024; PAN; 1.
PRINTS; PR00018; KRINGLE.
SMART; SM00130; KR; 2.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth factor;
SIGNAL 1
CHAIN 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HEPATOCYTE GROWTH FACTOR-LIKE/MACROPHAGE STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                          TRYPSIN FAMILY.
EMBL; X84043; CAA58862.1;
HSSP; P00747; 1CEA.
MEROPS; S01.977; -.
                                                                                                                                                               Thery C., Sharpe M.J., Batley S.J., "Expression of HGF/SF, HGF1/MSP and during early chick development."; Dev. Genet. 17:90-101(1995).
                                                                                                                                                                                                                                                                                                                                                                                                           HGF1/MSP.
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003609; Pan_app.
                   InterPro;
InterPro;
                                                                                                                                                                                                                                                                    TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90865;
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                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                         Archosauria;
                                                                                                                                                                                                                                            MEDLINE=96029010; PubMed=7554499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                             SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
IPR001314; iPR000001; iPR003014;
                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
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128
211
32
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                                                                                                                                                                                                                                                                                                                                                                       Aves;
                                                                                                                                                                                                                                                                                         N.A.
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                                                                                                                                                                                                                                                                                                                                                                         Neognathae;
                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.6%;
100.0%;
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               Chymotrypsin.
Kringle.
    PAN
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KRINGLE 1 (BY SIMILARITY).
KRINGLE 2 (BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
                                                                                                                                             PEPTIDASE
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Pred. No. 1.1e-140;
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c-met
                                                                                                                                             FAMILY
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                                                                                                                                                                                                     C.D., Ghe
                                                                                                                                             S1;
                                                                                                                                                                                                                                                                                                                                                                           Phasianidae;
                                                                                                                                             ALSO
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                                                                                                                                             KNOWN
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                                                                                                                                                                                                          functions
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Best Local
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PRINTS; PRO0018; KRINGLE.
SMART; SM00130; KR; 4.
SMART; SM00473; PAN_AP; 1.
SMART; SM00473; PAN_AP; 1.
SMART; SM00020; TRYP_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS500240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
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                                                                  644
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                                                                              KIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHKII
                                                                                                                                                                    GYEVHLGTLFKDPSPTDPDLQAIPIVRIICGPSESHLVLLKLAWPAVLNKRVALICLPPE
                                                                                                                                SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIV-NLDHPVI-SCAK-
| :|||||:||||| | | | | | | | | | :
| HLEKNYCRNPDNDSHGPWCYTMDPRTPFDYCAIKPCSGSAVPSVLENADAVTFEECGRR
                                                                                                                                                                                                                                                                                                                         HIRRCDDELDAEECYHGHGERYHGHVSKTRKGITCQRWDATTP----HVPQISPTTHPEA
                                                                                                                                                                                                                                                                                                                                          QIPNCDMS-HGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI-----FWEPDA
                                                                                                                                                                                                                                                                                                                                                                                         CRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLE-TTECIQGQGEGYRGTVN
                                                                 RAGVGACEGDYGGALACLTADCWVLEGVITPSRVCARTDQPALFIRVSLYVDWIHKVM
                                                                                                                                                                                DYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDFVSTIDLPNY
                                                                                                                                                                                                                      DERLOCKORVVGGMP--GNSPWTVSIRNRAGLHFCGGSLVKEQWVISTQQCFSSCDADLS
                                                                                                                                                                                                                                                                                                                                                                             TVSGIPCQRWDAQTLHRHHFVPSKYPCKDLQENYCRNPDGSEAPWCFTTRPGMRVAFCF
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                                                                                                                 RYIVPAGTTCEIAGFGETRGTADGHVLNVAKLPVMAHAECQAALRGR--LKESELCTAPL
                                                                                                                                                                                                                                    CRNPDSSEQPWCYTTDPALEREFCRIRVCKKRPR----PINVTTGCYRGKGEGYRGRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCGIKKCEDAVCMTCNGEDYRGFVDHTESGTECQRWDLQHPHKHPYHPDKYPEKGLDDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDKGFDDNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDTTERGLRCQHWQATTPHDHRFLPSLRNG--LEENYCRNPDRDKRGPWCYTVDPNVRHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- DCRAFHHERQSQLCQLLPWSQRSPGARLQKNIHYDLYQKKDFLRECIVANGTSYRGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLLSLAVALSAG - - - HRSPLNDFQRLRGTELRAAPNEPPPSAPAHGAAQQCAQRCANRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003609; Pan_app. IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease.
704 AA; 79341 MW; CABOD8CC41367C37 CRC64;
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.48;
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Pred. No. 1e-139;
 PRT;
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 296
 ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                 701
                                                                                                                                                                                                                                                                                                   489
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RESULT
P70521
 RRN OCC OCC RRN RRN RCC
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P70521
P70521;
P70521;
O1-FEB-1997 (TrEMBLrel. 02, Created)
T 01-FEB-1997 (TrEMBLrel. 02, Last sequence updat
DT 01-FEC-2001 (TrEMBLrel. 19, Last annotation upon accrophage STIMULATING PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0018; KRINGLE.
SMART; SM00130; KR; 2.
SMART; SM00473; PAN_AP; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS50070; KRINGLE_2; 2.
SEQUENCE 296 AA; 34546 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative Transcript.";
Science 0:0-0(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          014519;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
COMPETITIVE HGF ANTAGONIST.
           SEQUENCE FROM
                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR00309; Pan_app.
Pfam; PF00051; Kringle; 2.
Pfam; PF00024; PAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
TISSUE=LIVER;
                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M77227; AAA35980.1;
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chan A.M.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                          TKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYE 120
                                                                                                                                                                                                             HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNT
                                                                                                                                                                                                                                                                                                   NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP 180
                                                                                                                                                                                                  HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKNMRDIT
                                                                                                                                                                                                                                                       RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTP
                                                                                                                                                                                                                                            RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTP
                                                                                                                                                                                                                                                                                       NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 98.0
88; Conservative
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                                          Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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Pred. No. 5.9e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                          Craniata; Vertebrata; E
Sciurognathi; Muridae;
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                                                      Euteleostomi;
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                                            Murinae;
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Best Local S
Matches 315
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PRINTS; PRO018; KRINGLE.

R SMART; SM00130; KR; 4.

R SMART; SM00473; PAN_AP; 1.

R SMART; SM00020; Tryp_SPc; 1.

R PROSITE; PS00021; KRINGLE_1; 4.

R PROSITE; PS50070; KRINGLE_2; 4.

R PROSITE; PS50240; TRYPSIN_DOM; 1.

SEQUENCE 716 AA; 80733 MW; 06B7DF3EF56D921F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of Rat Macrophage-stimulating involvement in the Male Reproductive System."; Biochem. Biophys. Res. Commun. 227:273-280(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00747; 1K
MEROPS; S01.975;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97011126; PubMed=8858136;
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 536
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srPro; IPR003609; Pan_app.
srPro; IPR001254; Trypsin.
srpF00051; kringle; 4.
spF00024; PAN; 1.
spF00024; PAN; 1.
spF00089; trypsin; 1.
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                                                                                                                                                                              TDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHI 426
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                                                                                                                                                                                                                                          GQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCFT
                                                                                                                                                                                                                                                                                         LKDNYCRNPDASERPWCYTTDPNVEREFCDLPSCGPNLPPTTKGSKSQQRNKVKASNCFR
                                                                                                                                                                                                                                                                                                             FDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-----TMNDTDVPLETTECIQ
                                                                                                                                                                                                                                                                                                                                                                                                                     SYRGTVARTADGLECQAWSRREPNDHKYTPTPKNG--LEENECRNPDGDERGPWCYTTNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHLLLLPIAIPYAEGQRKRRNTIHEFKKSAKTTLIK-IDPALKIKTKK-VNTADQCANRC
FPS--RDLKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDF
                               QVQFEKCGKRVDQSNRLRVVGGHP--GNSPWTVSLRNRQGQHFCGGSLVKEQWVLTARQC
                                                  ----ISCAK----TKQLRVVNGIPTRTNIGWMVSLRYR-NKHICGGSLIKESWVLTARQC
                                                                                               FTPTSAPHAGLEANFCRNPDGDSHGPWCYTLDPETLFDYCALKRCDDDQPPSI--LDPPV
                                                                                                              FWEPDA--SKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHPV
                                                                                                                                                           SRPGLRVAFCYQIPRCTEEVVPEGCYHGSGEQYRGSVSKTRKGVQCQHW--SSETPHKPQ
                                                                                                                                                                                                                           GKGEDYRGTTNTTSAGVPCQRWDAQNPHQHRFVPEKYACKDLRENFCRNPDGSEAPWCFT
                                                                                                                                                                                                                                                                                                                                                     SVRFQSCGIKSCREAVCVWCNGEDYRGEVDVTESGRECQRWDLQHPHSHPFHPEKFPDKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPLLLLAQCSRALGQ----RSPLNDFQLLRGTELRNLLHPVVPGPWQEDVADAEECARRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR0001314; Chymotrypsin. IPR000001; Kringle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.1%; Score 1615; DB 11;
43.3%; Pred. No. 1.3e-138;
tive 118; Mismatches 254;
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Best Local (
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Q91XG8;
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da EMBL; BC010551; AAH10551.1; -. SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEPATOCYTE GROWTH FACTOR-LIKE
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 412
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                                                                                                                         QGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGSESPWCF
                                                                                                                                                                                                                                                                                                                                                                                LPLLLLLVQCSRALGQRSPLNDFQLFRGTELRNLLHTAVPGP-----WQEDVADAEECARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESEICAGAEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYA 713
QFTPTSAPQAGLEANFCRNPDGDSHGPWCYTLDPDILFDYCALQRCDDDQPPSILDPPDQ
            IFWEPDASK--LNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNLDHP
                                                                  TTDPNIRVGYCSQIPNC-DMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRH
                                                                                                                                                              DLKDNYCRNPDGSERPWCYTTDPNVEREFCDLPSCGPNLPPTVKGSKSQRRNKGKALNCF
                                                                                                                                                                             GFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADN-----TMNDTDVPLETTECI
                                                                                                                                                                                                                               PEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRHKFLPERYPDK
                                                                                                                                                                                                                                                                     VSYRGTVARTAGGLPCQAWSRREPNDHKYTPTPKNG--LEENFCRNPDGDPRGPWCYTTN 173
                                                                                                                                                                                                                                                                                   RSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSN 193
                                                                                                                                                                                                                                                                                                                                                      CTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLN
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                                                                                                        RGKGEDYRGTINTTSAGVPCQRWDAQSPHQHRFVPEKYACKDLRENFCRNPDGSEAPWCF
                                                                                                                                                                                                                  RSVRFQSCGIKTCREAVCVLCNGEDYRGEVDVTESGRECQRWDLQHPHSHPFQPEKFLDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                           -GPLLDCRAFHYNMSSHGCQLLPWTQHSLHTQLYHSSLCHLFQKKDYVRTCIMDNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1605; Di
Pred. No. 1.1e
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Veri
Sciurognathi;
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1.1e-137;
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Best Loca
Matches
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HEPATOCYTE G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Early expression of zebrafish Hepatocyte Growth Factor-
suggests a conserved role in vertebrate neural induction
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF370035; AAK54207.1; -.
SEQUENCE 709 AA; 81271 MW; 9907236C5DB73A20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brachydanio rerio (Zebrafish) (Zebra dai
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
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Bassett D.I., Wilson
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                                                                                                                                                                                                                                                                     EGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTPHRH
                                                                                                                                                                                                                                                                                                                                                                                   YIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MLFFLTALLLRLDSVDGY---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MINKVM
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                         RSSYTTNCFRGRGEDYRGKVNETTSGIPCQRWDAQKPHEHPFFPKTYECKGLEENYCRNP
                                                                                                                                                                                     KFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPLE--
                                                                                                                                                                                                                                            RIGPWCYTTDPERRYESCNIPQCKDEVCITCNGEDYRGQVDHTISGKECQRWDQQFPHQH
                                                                                                                                                                                                                                                                                                                                                         YVRKCIVGKGEDYRGKVSTTTSGRTCQQWWSKFPHDHRWTPSATNGLEL--NYCRNPDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEDCAKRCTESP - - - - ECRAFNYEFRPSLVCKHLPWVGDGDNADVKRNV - - NCDLYEMKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADOCANRCTRNKGLPFTCKAFVFD-KARKQCLWFPF--NSMSSGVKKEFGHEFDLYENKD
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                                                   -TTECIOGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNP
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Pred. No. 2
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?.5e-135;
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Euteleostei;
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RESULT
018783
Pfam; PF00024; PAN; 1.

Pfam; PF00024; PAN; 1.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00718; KRINGLE.

SMART; SM00473; PAN_AP; 1.

SMART; SM00473; PAN_AP; 1.

SMART; SM00473; FAN_AP; 1.

SMART; SM00473; FAN_BP; 1.

SMART; SM00473; TRYPSIN_LE 1; 5.

PROSITE; PS00021; KRINGLE 2; 5.

PROSITE; PS50070; KRINGLE 2; 5.

PROSITE; PS50070; KRINGLE 2; 5.

PROSITE; PS500740; TRYPSIN_DOM; 1.

PROSITE; PS500134; TRYPSIN_LIS; 1.

PROSITE; PS00134; TRYPSIN_ER; 1.

Hydrolase; Serine protease.

SEQUENCE 806 AA; 90981 MW; 95
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018783;
01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
HSSP;
                                                                                                                                                                                                                                                                  InterPro; IPR003609; Par
InterPro; IPR001254; Try
Pfam; PF00051; kringle;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawn R.M., Schwartz K., Patthy L.; "Convergent evolution of apolipoprotein(a) in primates Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KITRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98004511; PubMed=9342350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macropus eugenii (Tammar wallaby).
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                                                                                                                                                                                                                                                                                                                             InterPro; IPR003014;
                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001314; InterPro; IPR000001;
                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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; LENGTH: 728 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-815-333A-2

Query Match 100.0%; Best Local Similarity 100.0%; Matches 728; Conservative 0;

Score 4126; Pred. No. 0; 0; Mismatches

DΒ 0;

Length

728; 0;

Gaps

0

NAME: Green, Robert F.
REGISTRATION NUMBER: 2755
REFERENCE/DOCKET NUMBER: 4406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
TELEFAX: (312) 616-5700
TELEFAX: 25-353
INFORMATION FOR SEQ ID NO: 2:

44069

APPLICATION NUMBER: US/0: FILING DATE: 19911227 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:

US/07/815,333A

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•	ALIGNMENTS US/07815333A Toshikazu , Kunio EPITHELIOCYTE GROWTH ACCELERATOR 2 S: Voit & Mayer tial Plaza, Suite 4900 ates of America M: y disk ompatible ompatible pC-DOS/MS-DOS Release #1.0, Version #1.25 ATA: US/07/815 3334	AL TION: TION: TION: TION: TENTION: TENTIFICATION: TENTIFICATION NATION: TENTIFICATION NATION: TENTIFICATION NATION: TENTIFICATION NATION: TENTIFICATION NATION TENTIFICATION TENTIFICATION TO PROBLE TO PROBLE TO PATE TO T	T 1 -815-33A-2 -815-33A-2 -ent No. 5342831 NERAL INFORMATION: APPLICANT: Matsumoto, Ku TITLE OF INVENTION: EPIT NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSE: Leydig, Voi STREET: Two prudential CITY: Chicago STATE: Illinois COUNTRY: United States COUNTRY: United States TOUNTER READABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: IBM PC Compa OPERATING SYSTEM: PC-DI SOFTWARE: Patentin Rel CURRENT APPLICATION DATA: ADDLICATION DATA:	SULT 1 2-07-815-333A-2 Sequence 2, Applicati Patent No. 5342831 GENERAL INFORMATION: APPLICANT: Maksum APPLICANT: Matsum TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD STREET: Two pru CITY: Chicago STATE: Illinois COUNTRY: United ZIP: 60601 ZIP: 60601 COMPUTER READABLE MEDIUM TYPE: F1 COMPUTER: IBM E OPERATING SYSTEM SOFTWARE: Paten CURRENT APPLICATION ADBLICATION SUMB	RESULT 1 US-07-815- Sequence Patent N Patent N PATENT RPPLI
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Sequence 22, Application U
; Patent No. 5547856
; GENERAL INFORMATION;
GORDONSKI, F
                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb floor for the following form of the floor floo
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HE NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                      Lokker, Nathalie A., Mark, Melanie E GROWTH FACTOR VARIANTS
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REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0755779P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-4416
TELEPHONE: 415/225-4416
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
Type:
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; TOPOLOGY: Linear
US-08-087-783A-22
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Best Local Sim
Matches 728;
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APPLICATION NUMBER: 07/884
FILING DATE: 18-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/885
FILING DATE: 18-MAY-92
ATTORNEY/AGENT INFORMATION:
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AEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHKII
                                                   ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMMDKNME
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Pred. No. 0;
0; Mismatches
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US-07-838-410-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/JP
FILING DATE: 15-JUL-1991
PRIOR APPLICATION NUMBER: JP 185
APPLICATION NUMBER: JP 185
FILING DATE: 13-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN L
REGISTRATION NUMBER: 17,74
                                                                                                                                                                                                                                                                                        TELEX: 64191
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/838,410
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                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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ORGANISM:
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ORIGINAL SOURCE:
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CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
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721 LTYKVPQS 728
NAME/KEY: Protein
LOCATION: 490..505
OTHER INFORMATION: 0
                                                                                          NAME/KEY: Domain
LOCATION: 393..405
OTHER INFORMATION: OTHER INFORMATION: 9
                                                                                                                                                                                                                                                         STRANDEDNESS: single TOPOLOGY: linear
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TELEFAX: 703-243-6410
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                                                                                                                                                                                    TYPE:
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OOGAKI, FUMIKO
TAKAOKA, HIROAKI
TSUDA, EISUKE
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/note= "N-TERMINAL AMINO SEQUENCE OF BETA-CHAIN"
                                                                                          /note= "INTERNAL AMINO ACID
SEQUENCE IN ALPHA-CHAIN"
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COARTION: 605.623
COTHER INFORMATION: 5:
OTHER INFORMATION: 5:
US-07-838-410-1
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                                                                                                    AEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHKII 720
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                                                                                                                                                                    NYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEICAG
                                                                                                                                                                                                                                                                             DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRD
                                                                                                                                                                                                                                                                                                                                 DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
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                                                                            LTYKVPQS 728
                                                                                                                                                          NYGCTIPEKTSCSVYGWGYTGLINYDGLLRVAHLYIMGNEKCSQHHRGKVTLNESEICAG
                                                                                                                                                                                                                                                                DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRD
                                                                                                                                                                                                                                                                                                                    DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
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99.3%;
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Sequence 1, Application US/08290937B Patent No. 5648233

GENERAL INFORMATION: APPLICANT:
APPLICANT: APPLICANT:

YAMAGUCHI, KYOJ SHIMA, NOBUYUKI MURAKAMI, AKIHIKO MASAAKI

KYOJI

GOTO,

APPLICANT: APPLICANT: APPLICANT:

MASUNAGA, HIROAKI TAKAHIRA, REIKO TSUDA, EISUKE

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Best Local Similarity
Matches 723; Conserv
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APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANJI
TITLE OF INVENTION: MODIFIED TCF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
08-290-9378-1
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: FJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
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MEDIUM TYPE: Floppy disk
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                           1 MWVTKLLPALLLQHVLLHLLLLPIAIPYAEGQRKRRNTIHEFKKSAKTTLIKIDPALKIK 60
             ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME 420
                                                           ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS 360
                                                                                                                           HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL 300
                                                                                                                                                                                          RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTP 240
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ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME
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Query Match
Best Local Similarity
Matches 723; Conserv

Conservative

99.1%; 99.3%;

Score 4088.5; Pred. No. 0; 0; Mismatches

DB 0,:

723; υ ()

Indels Length

Gaps

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; TOPOLOGY: 1;; MOLECULE TYPE: US-08-404-643-1
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                                                                                                                       TELEFAX: (617)-248-7100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          FILING DATE: 15-MAR-1995
CLASSIFICATION: 436
ATTORIEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,50
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: SHIMA, NOBUYUKI
APPLICANT: OOGAKI, FUMIKO
                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELEPHONE: (617)-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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CITY: BOSTON
STATE: MA
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                                                 TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ ADDRESSEE: THIBEAULT
                                                                                       LENGTH:
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                                                                                     723 amino acids
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                                  linear
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                                                                                                                                                                                                                                                                                                                                    Version
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Sequence 1, Application US/09194326
Patent NO. 6306827
GENERAL INFORMATION:
APPLICANT: KINOSAKI, Masahiko
APPLICANT: Ogawa, Hiromi
APPLICANT: Wasanuga, Hiromi
APPLICANT: Wasanuga, Hiromi
APPLICANT: Wasanuga, Hiromi
APPLICANT: Wasanuga, Hiromi
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Higashio, Kanji
TITLE OF INVENTION: Agent for Preventing and/
FILE REFERENCE: FUN-069
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: PCT/JP98/01221
EARLIER APPLICATION NUMBER: JP98-01-20
EARLIER APPLICATION NUMBER: JP98-03-20
EARLIER FILING DATE: 1998-03-28
NUMBER OF SEQ ID NOS: 3
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                                                                                                  Disease
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; SOFTWARE: PatentIn Ve
; SEQ ID NO 1.
; LENGTH: 723
; TYPE: PRT
: ORGANISM: HOMO Sapie
; FEATURE:
; OTHER INFORMATION: T
US-09-194-326-1
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Best Local Sim
Matches 723;
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                                                                     LTYKVPQS
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                                                                                                                                                         LKDYEAWLGIHDVHGRGDEKCKQVLNVSQLVYGPEGSDLVLMKLARPAVLDDEVSTIDLP
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99.3%;
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Pred. No. 0;
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APPLICANT:
APPLICANT:
APPLICANT:

MURAKAMI, AKI GOTO, MASAAKI

EISUKE

NOBUYUKI

AKIHIKO

APPLICANT:

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,937B
FILING DATE: 19-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,303
REFERENCE/DOCKET NUMBER: 32,003
REFERENCE/DOCKET NUMBER: 5JN-022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity Matches 722; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MASUNAGA, HIROAKI
APPLICANT: TAKAHIRA, REIKO
APPLICANT: OGGAKI, FUMIKO
APPLICANT: UEDA, MASATSUGU
APPLICANT: HIGASHIO, KANJI
TITLE OF INVENTION: MODIFIED TONOMBER OF SEQUENCES: 13
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ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
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MEDIUM TYPE: Floppy disk
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361
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                                                                                                                                                                                                                                                                                                                                                                  RGEEGGPWCFTSNPEVRYEVCDIPQCSEVECMTCNGESYRGLMDHTESGKICQRWDHQTP 240
                                                                                                                                                                                                                               NKDYIRNCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNP 180
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ESPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYRGNGKNYMGNLSQTRSGLTCSMWDKNME
                               ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS
                                                ETTECIQGQEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS 360
                                                                                                HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL
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Pred. No. 0;
1; Mismatches
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patent No. 5648233
GENERAL INFORMATION:
APPLICANT: YAMAGUCI
APPLICANT: SHIMA, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-08-290-937B-3
                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPHANE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,5
REFERENCE/DOCKET NUMBER:
                       SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 DHPVISCAKTKQLRVVNGIPTRTNIGWMVSLRYRNKHICGGSLIKESWVLTARQCFPSRD 540
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                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
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                                                                                                                                                                                                          APPLICATION NUMBER:
STRANDEDNESS:
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               amino acid
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TAKAHIRA, REIKO
OOGAKI, FUMIKO
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TSUDA, EISUKE
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SHIMA, NOBUYUKI
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32,503
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; MOLECULE TYPE:
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Best Loc
Matches
          GENERAL INFORMATION:
APPLICANT: Komiyam
APPLICANT: Nakahat
APPLICANT: Kubo, T
APPLICANT: Tanaka,
APPLICANT: Kawano,
                                                                        Sequence 3, Application Patent No. 6221359
                                                                       Patent No.
  APPLICANT:
                                                                                                                                     716
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                                                                                                                                                                            AEKIGSGPCEGDYGGPLVCEQHKMRMVLGVIVPGRGCAIPNRPGIFVRVAYYAKWIHKII
                  Nakahata, Tat
Kubo, Tetsuo
Tanaka, Ryuhe
          Kawano,
                                                 Komiyama, Atsushi
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Tetsuo
                    Ryuhei
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99.0%;
                                                                                 US/08030410
                                         Tatsutoshi
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TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local S
Matches 720
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NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kojima, Katsuaki
TITLE OF INVENTION: HEMOPOIETIC
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DLHRHIFWEPDASKLNENYCRNPDDDAHGPWCYTGNPLIPWDYCPISRCEGDTTPTIVNL
                                                                                                                                 ETTECIQGQGEGYRGTVNTIWNGIPCQRWDSQYPHEHDMTPENFKCKDLRENYCRNPDGS
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T: 400 Garden City Plaza
Garden City
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nilarity 98.9%;
Conservative
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Pred. No. 0;
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APPLICANT: KINGSAKI, MASAHIKO
APPLICANT: KONGSAKI, MITOMI
APPLICANT: MASANUGA, HITOMI
APPLICANT: MASANUGA, HITOMI
APPLICANT: KOBAYASHI, FUNIE
APPLICANT: KOBAYASHI, FUNIE
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: YAMAGUCHI, KYOJI
APPLICANT: YAMAGUCHI, KYOJI
TITLE OF INVENTION: ASPANT APPLICATION NUMBER: US/09/194,326
CURRENT APPLICATION NUMBER: DET/JP98/01221
EARLIER APPLICATION NUMBER: PCT/JP98/01221
EARLIER APPLICATION NUMBER: JP 94989
EARLIER APPLICATION NUMBER: JP 94989
EARLIER FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
Matches 719; Conserv
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LENGTH: 723
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: RKRR2AAAA OTHER INFORMATION: mutant of TCF-II 09-194-326-2
                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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 HRHKFLPERYPDKGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADNTMNDTDVPL
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APPLICANT: Kinosaki, Masahiko
APPLICANT: Ogawa, Hiromi
APPLICANT: Masanuga, Hiroaki
APPLICANT: Masanuga, Hiroaki
APPLICANT: Kobayashi, Funde
APPLICANT: Kobayashi, Funde
APPLICANT: Yamaguchi, Kyoji
APPLICANT: Higashio, Kanji
CURRENT GFINVENTION: Agent for Preventing and/or Treating Renal Disease
FILE REFERENCE: FJN-069
CURRENT APPLICATION NUMBER: US/09/194,326
CURRENT FILING DATE: 1998-11-24
EARLIER APPLICATION NUMBER: PCT/JP98/01221
EARLIER APPLICATION NUMBER: DT JP 94989
EARLIER FILING DATE: 1997-03-28
NUMBER OF SEQ ID NOS: 3
NUMBER OF SEQ ID NOS: 3
COMMERCE: DETAILS OF 2 0
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                                                                             ; OTHER INFORMATION: Description of Artificial Sequence:KIKKTKK27AIATAA; OTHER INFORMATION: mutant of TCF-II US-09-194-326-3
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LENGTH: 723
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
Query Match 98.1
Best Local Similarity 98.8
Matches 719; Conservative
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                                                                                                                                               ORGANISM: Artificial Sequence
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98.8%;
 Score 4064.5;
Pred. No. 0;
0; Mismatches
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US-08-460-890A-50
                                                                                                                                                                                                                                                              Patent No. 5994109
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth S
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Disket
                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Ly
                                                                                                                                                                   APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID
TITLE OF INVENTION: METHODS OF U.
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5. 5994109
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Best Local Similarity
Matches 697; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/855,389
FILING DATE: March 20,1992
APPLICATION NUMBER: PCT/US93/0:
FILING DATE: March 19,1993
ATTORNEY/AGENT INFORMATION:
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LENGTH: 697 amino acids
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FILING DATE: June 5, 1995
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STRANDEDNESS: sir
TOPOLOGY: linear
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
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SOFTWARE: FastSEQ
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COMPUTER: II
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                                                                         RYRNKHICGGSLIKESWVLTARQCFPSRDLKDYEAWLGIHDVHGRGDEKCKQVLNVSQLV 571
                                                                                                                                                     YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW 451
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                 RYRNKHICGGSLIKESWYLTARQCFPSRDLKDYEAWLGIHDVHGRGDEKCKQVLNVSQLV
                                                                                                                                        YRGNGKNYMGNLSQTRSGLTCSMWDKNMEDLHRHIFWEPDASKLNENYCRNPDDDAHGPW
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FastSEQ for Windows
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US-08-167-641C-50
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                                                               Matches
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: WOO, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Cortchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCT/US93/02725
FILING DATE: March 19, 1993
                                                                                                                                                                                                                                      TELEPHONE: (213) 489-160
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: pepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. I
                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon 6 Lyon STREET: 633 West Fifth S STREET: Suite 4700 CITY: Los Angeles STATE: Collfornia COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,327
REERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                              ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                            APPLICANT: WOO, SAVIO L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER
TITLE OF INVENTION: METHODS OF USE
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                             ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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   OPERATING SYSTEM: IBM P.C. DOS 5. SOFTWARE: FastSEQ for Windows 2.0 JRRENT APPLICATION DATA:
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APPLICATION NUMBER: FILING DATE: June 5

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APPLICATION NUMBER: PCT/US93/02725
FILING DATE: MATCH 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: WARDLING, RICHARD J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 212/063
TELECHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 495-1600
TELEST OF THE SECONDATION FOR SECONDATI
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PRIOR APPLICATION UMBER: 08/167,641
APPLICATION UMBER: 07/855,389
APPLICATION NUMBER: 07/855,389
TILING DATE: March 20, 1992
TILING DATE: March 20, 1992
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AHLYIMGNEKCSQHHRGKVTLNESEICAGAEKIGSGPCEGDYGGPLVCEQHKMRMVLGVI 691
                                                                                         YGPEGSDLVLMKLARPAVLDDFVSTIDLPNYGCTIPEKTSCSVYGWGYTGLINYDGLLRV 631
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER:
FILING DATE: Decembe
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OPERATING SYSTEM: IBM P.C. DOS 5.
SOFTWARE: FASTED for Windows 2.C
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 697 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: March 19, 1 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND TITLE OF INVENTION: METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07. FILING DATE: March 20. APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/462,040 FILING DATE: June 5, 1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
92 ARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKSGIKCQP
                                                                  32 QRKRRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDK 91
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
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633 West Fifth
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Gottchalk, Stephen
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December 14, 1993
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Search completed: June 18, 2002, 17:47:21 Job time: 242 sec